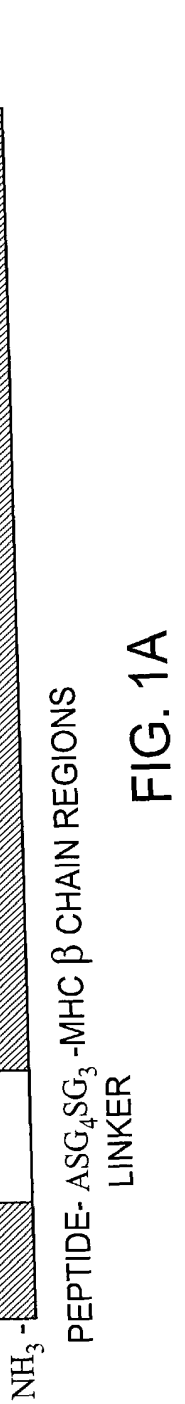
PEPTIDE-LINKER-β CHAIN CONSTRUCT
-COOH
NH_3 -
PEPTIDE- ASG_4SG_3 -MHC β CHAIN REGIONS
LINKER

FIG. 1A

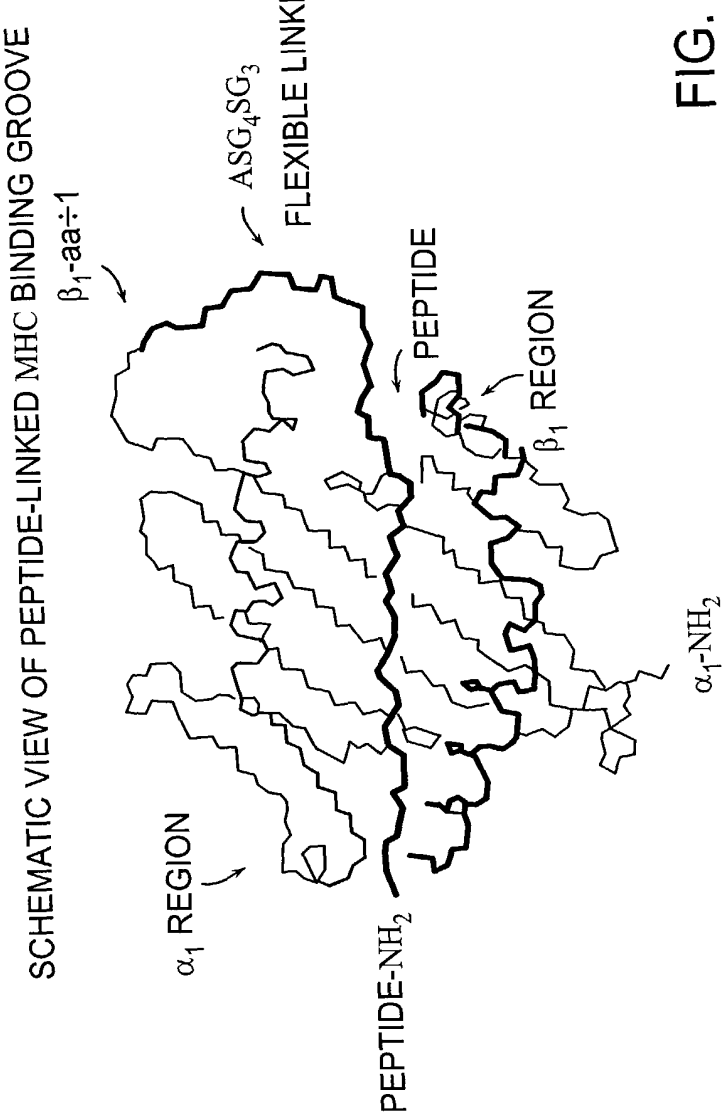
SCHEMATIC VIEW OF PEPTIDE-LINKED MHC BINDING GROOVE
β_1-aa÷1
ASG_4SG_3
FLEXIBLE LINKER
PEPTIDE
β_1 REGION
α_1 REGION
PEPTIDE-NH_2
α_1-NH_2

FIG. 1B

SCHEMATIC VIEW OF SOLUBLE PEPTIDE-LINKED MHC-IgG C-REGION FUSION PROTEIN

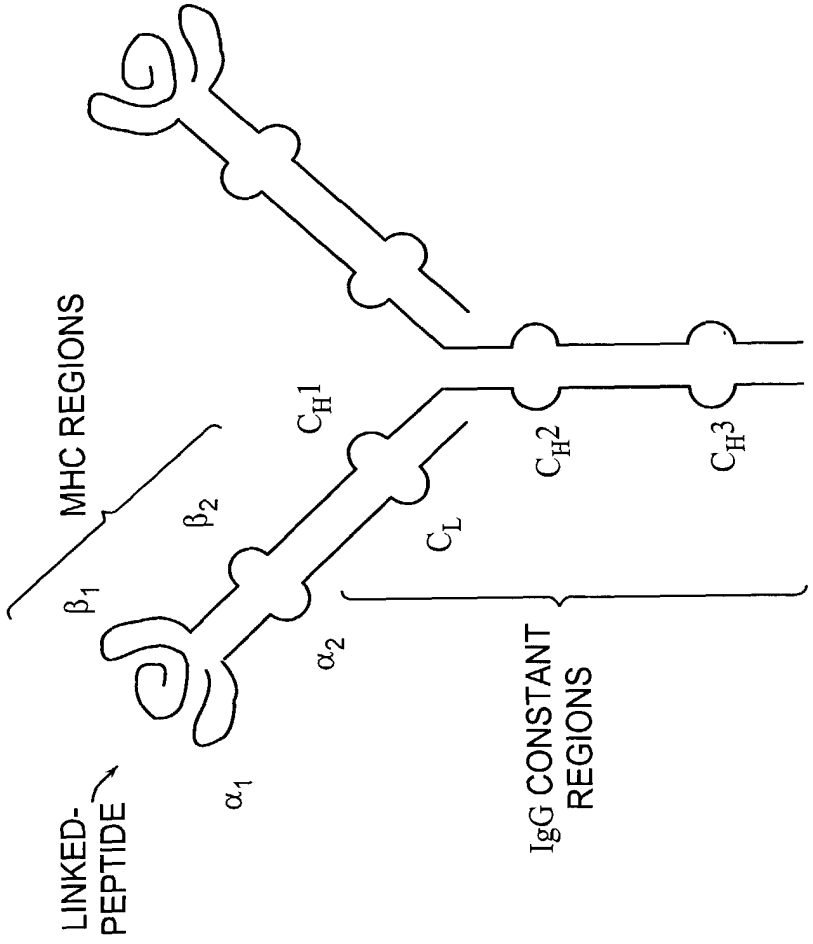

FIG. 1C

I-A ^{d} α CHAIN CLONING SCHEME

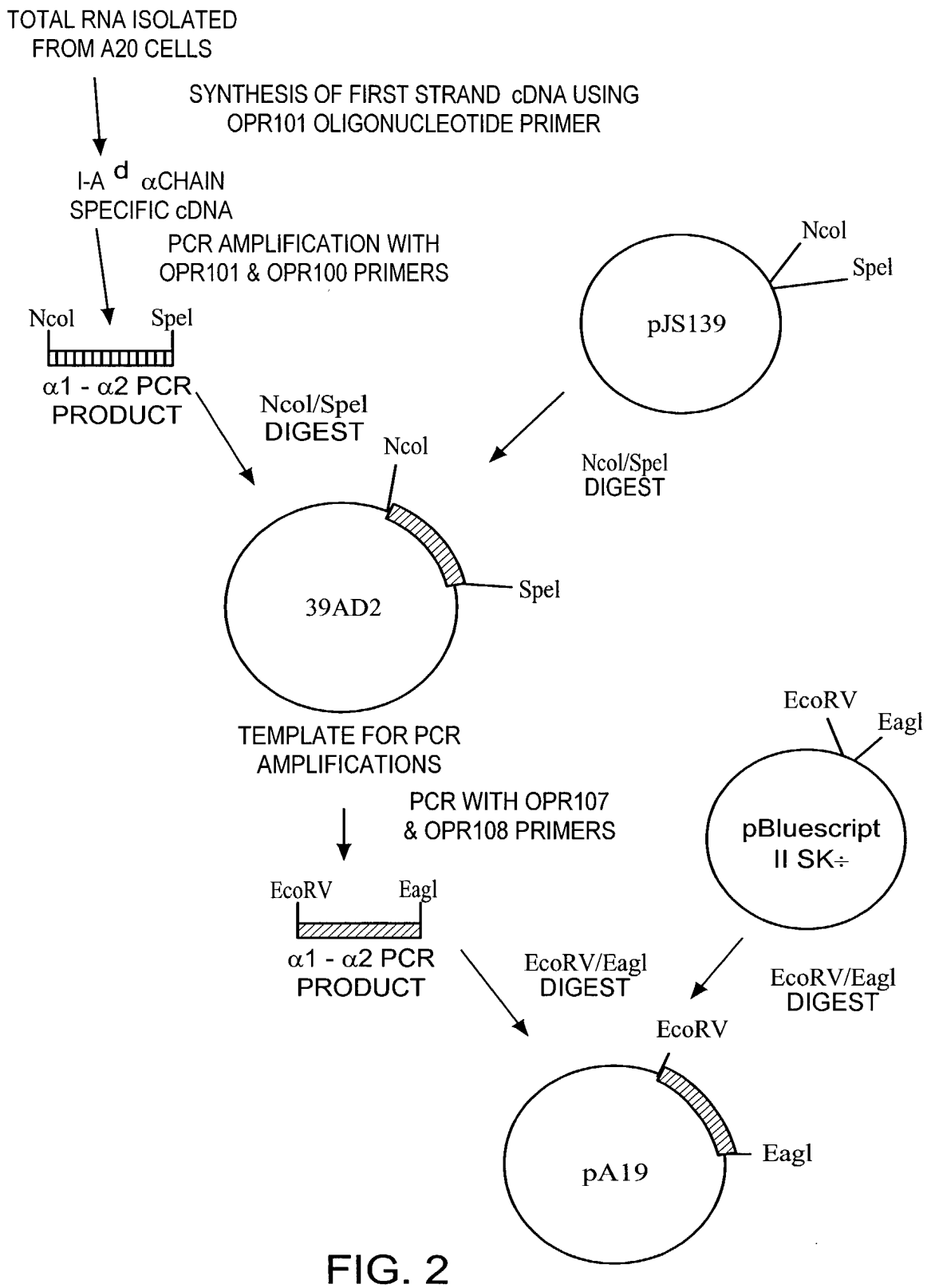

FIG. 2

I-A^d β CHAIN CLONING SCHEME

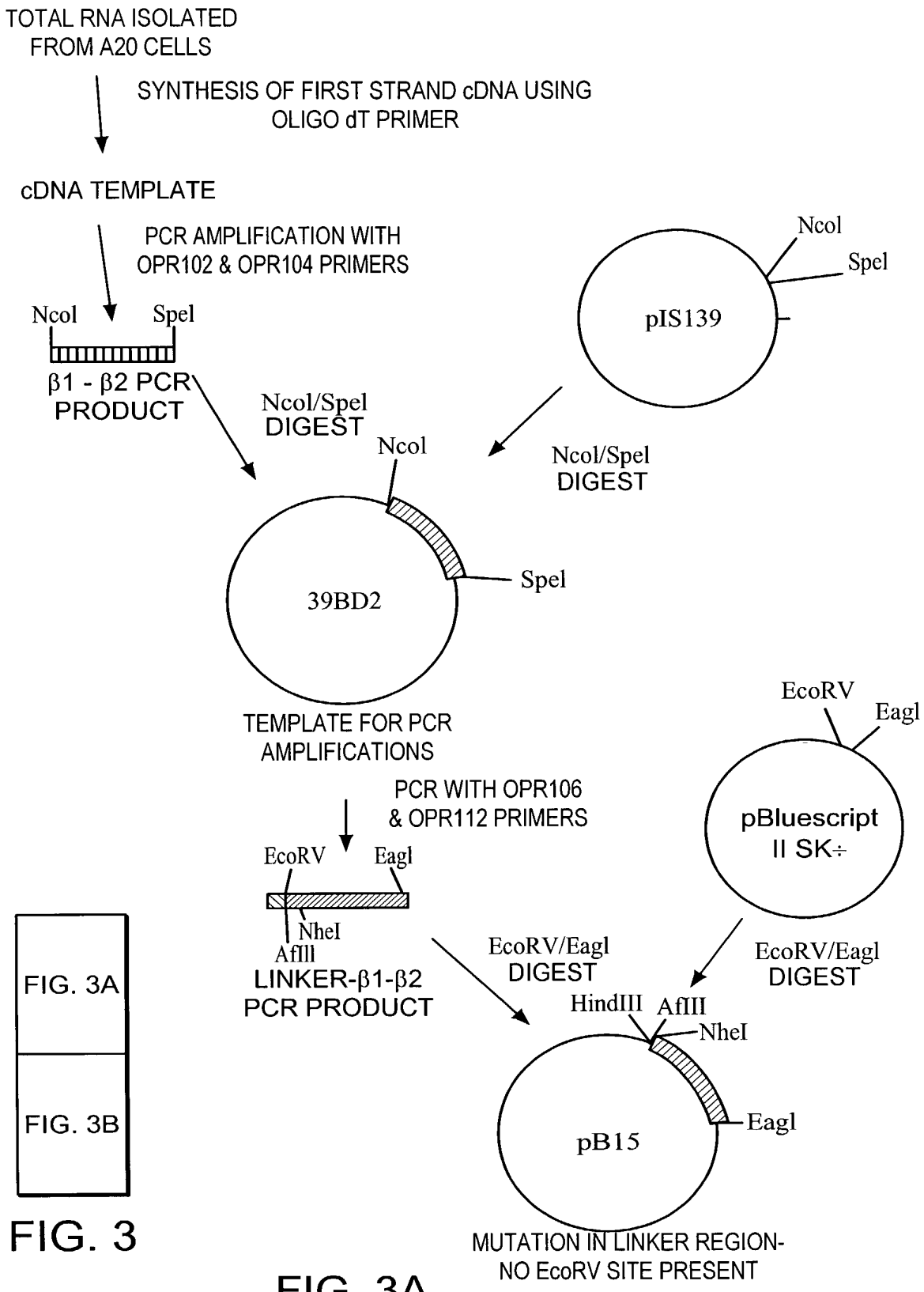

FIG. 3A

FIG. 3B

FIG. 3

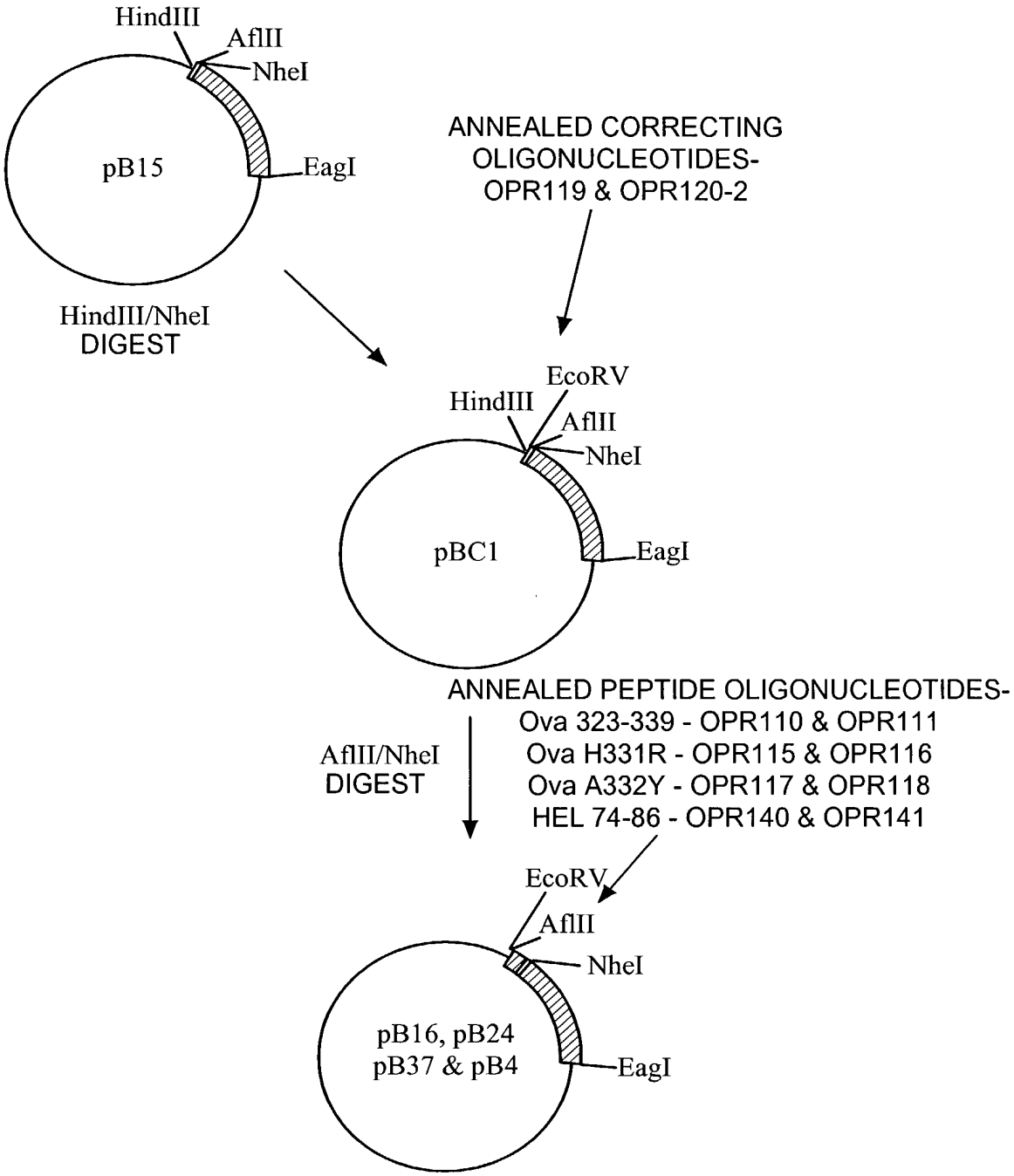
HindIII
AflII
NheI
pB15
EagI
HindIII/NheI
DIGEST
ANNEALED CORRECTING
OLIGONUCLEOTIDES-
OPR119 & OPR120-2
EcoRV
HindIII
AflII
NheI
pBC1
EagI
ANNEALED PEPTIDE OLIGONUCLEOTIDES-
Ova 323-339 - OPR110 & OPR111
Ova H331R - OPR115 & OPR116
Ova A332Y - OPR117 & OPR118
HEL 74-86 - OPR140 & OPR141
AflII/NheI
DIGEST
EcoRV
AflII
NheI
pB16, pB24
pB37 & pB4
EagI

FIG. 3B

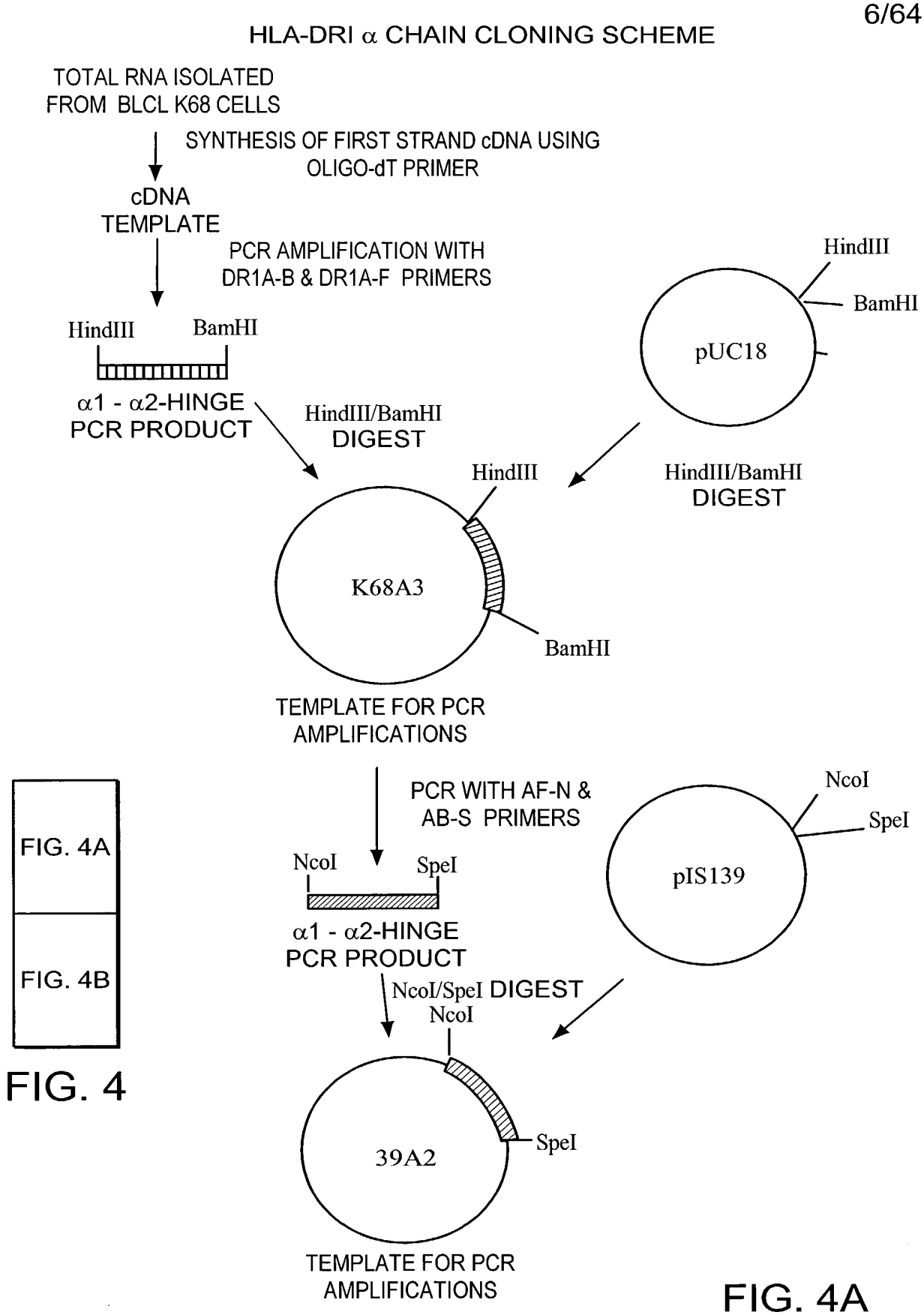

FIG. 4A

FIG. 4A

FIG. 4B

FIG. 4

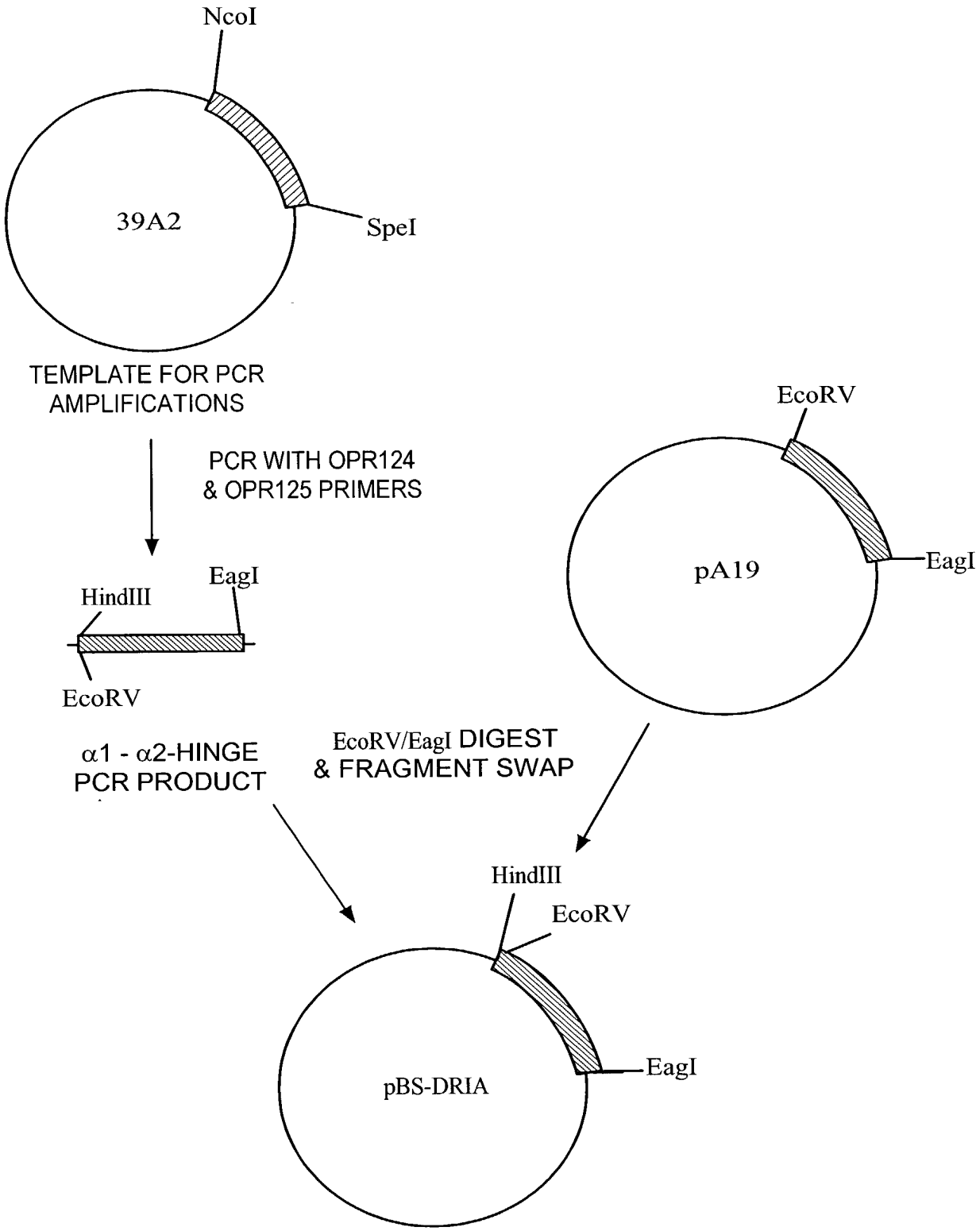
NcoI
39A2
SpeI
TEMPLATE FOR PCR AMPLIFICATIONS
PCR WITH OPR124 & OPR125 PRIMERS
HindIII
EagI
EcoRV
α1 - α2-HINGE PCR PRODUCT
EcoRV
pA19
EagI
EcoRV/EagI DIGEST & FRAGMENT SWAP
HindIII
EcoRV
pBS-DRIA
EagI

FIG. 4B

HLA-DRI β CHAIN CLONING SCHEME

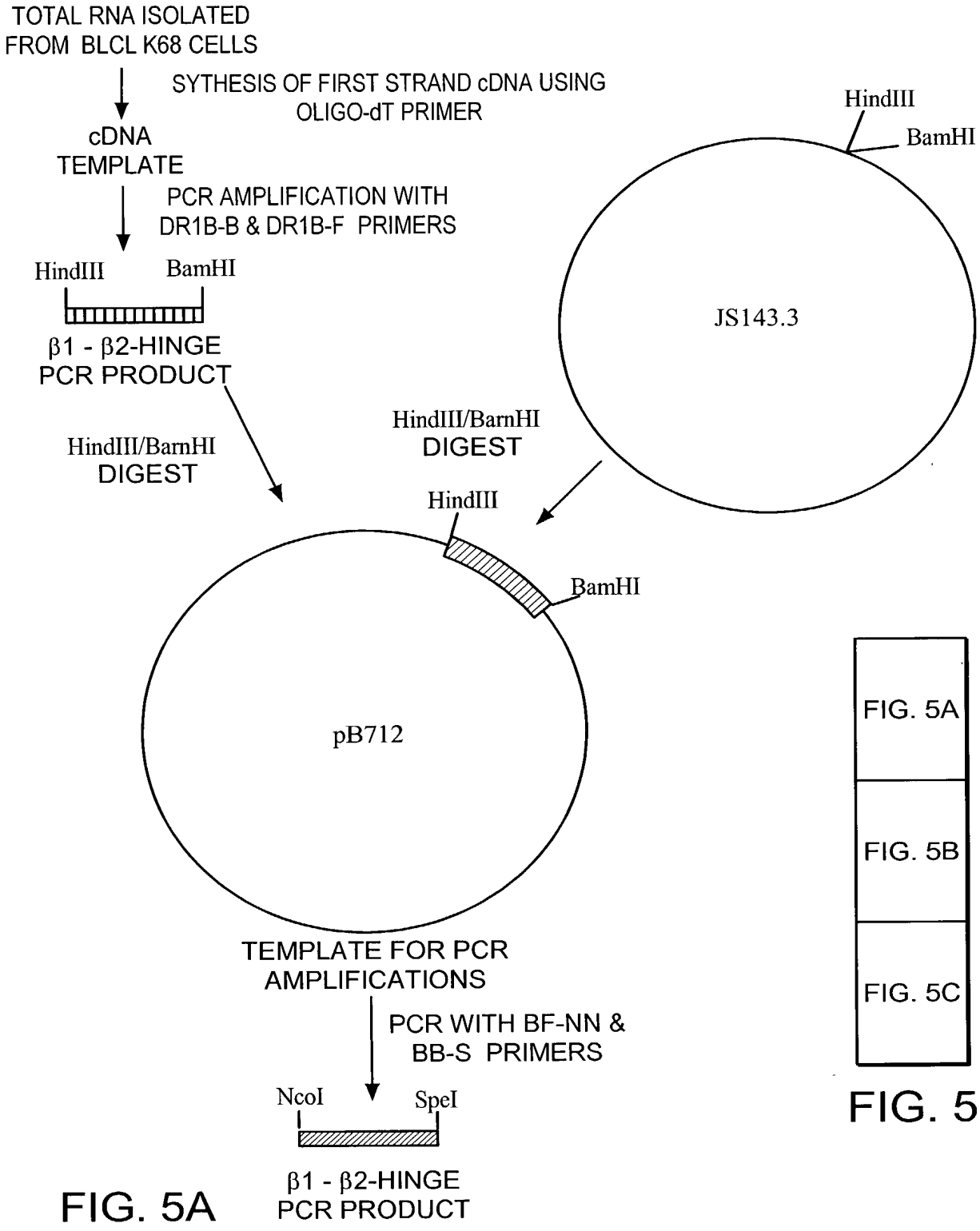

FIG. 5A

FIG. 5A
FIG. 5B
FIG. 5C

FIG. 5

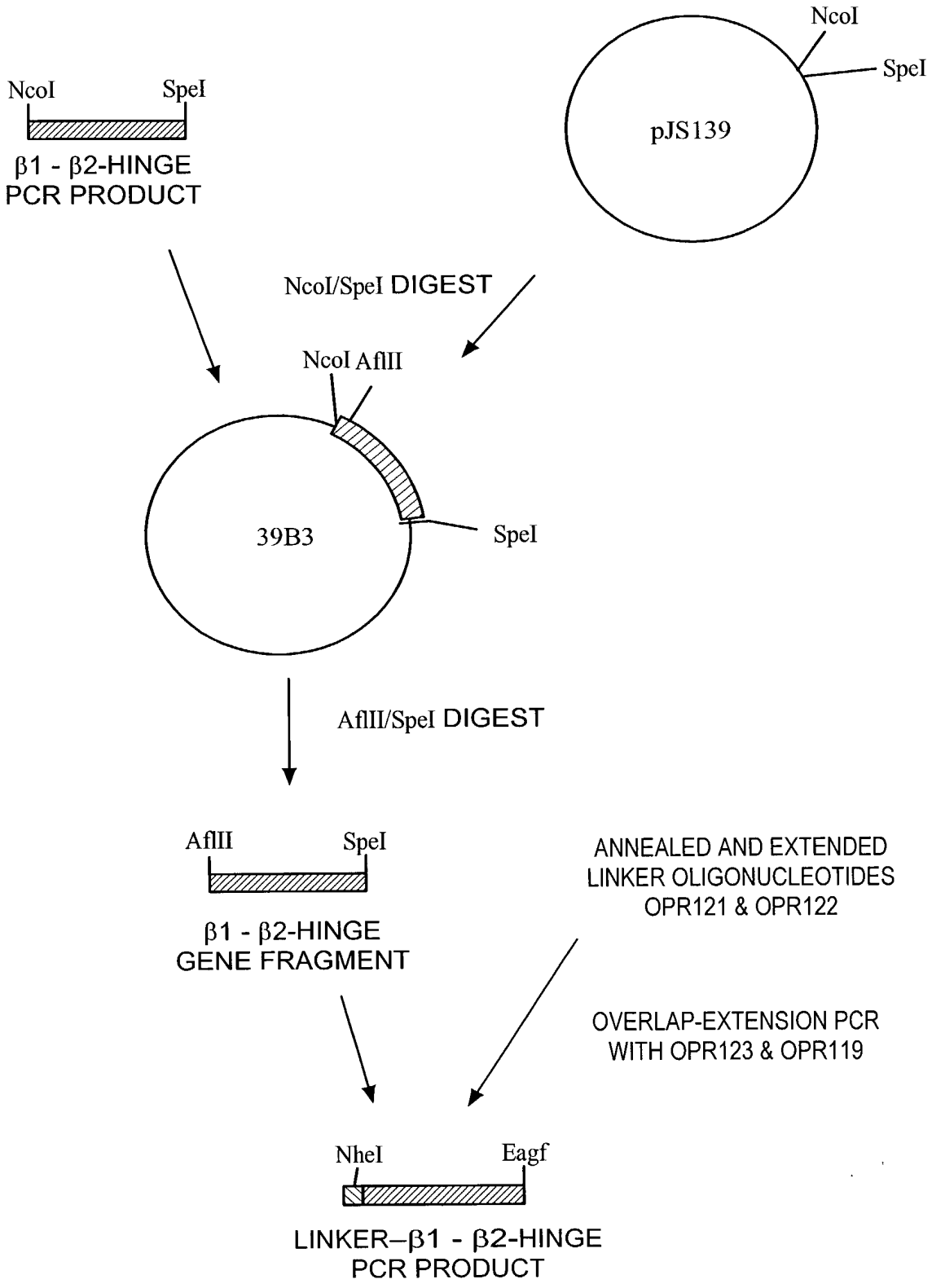
NcoI
SpeI
β1 - β2-HINGE
PCR PRODUCT
NcoI
SpeI
pJS139
NcoI/SpeI DIGEST
NcoI AflII
39B3
SpeI
AflII/SpeI DIGEST
AflII
SpeI
β1 - β2-HINGE
GENE FRAGMENT
ANNEALED AND EXTENDED
LINKER OLIGONUCLEOTIDES
OPR121 & OPR122
OVERLAP-EXTENSION PCR
WITH OPR123 & OPR119
NheI
Eagf
LINKER–β1 - β2-HINGE
PCR PRODUCT

FIG. 5B

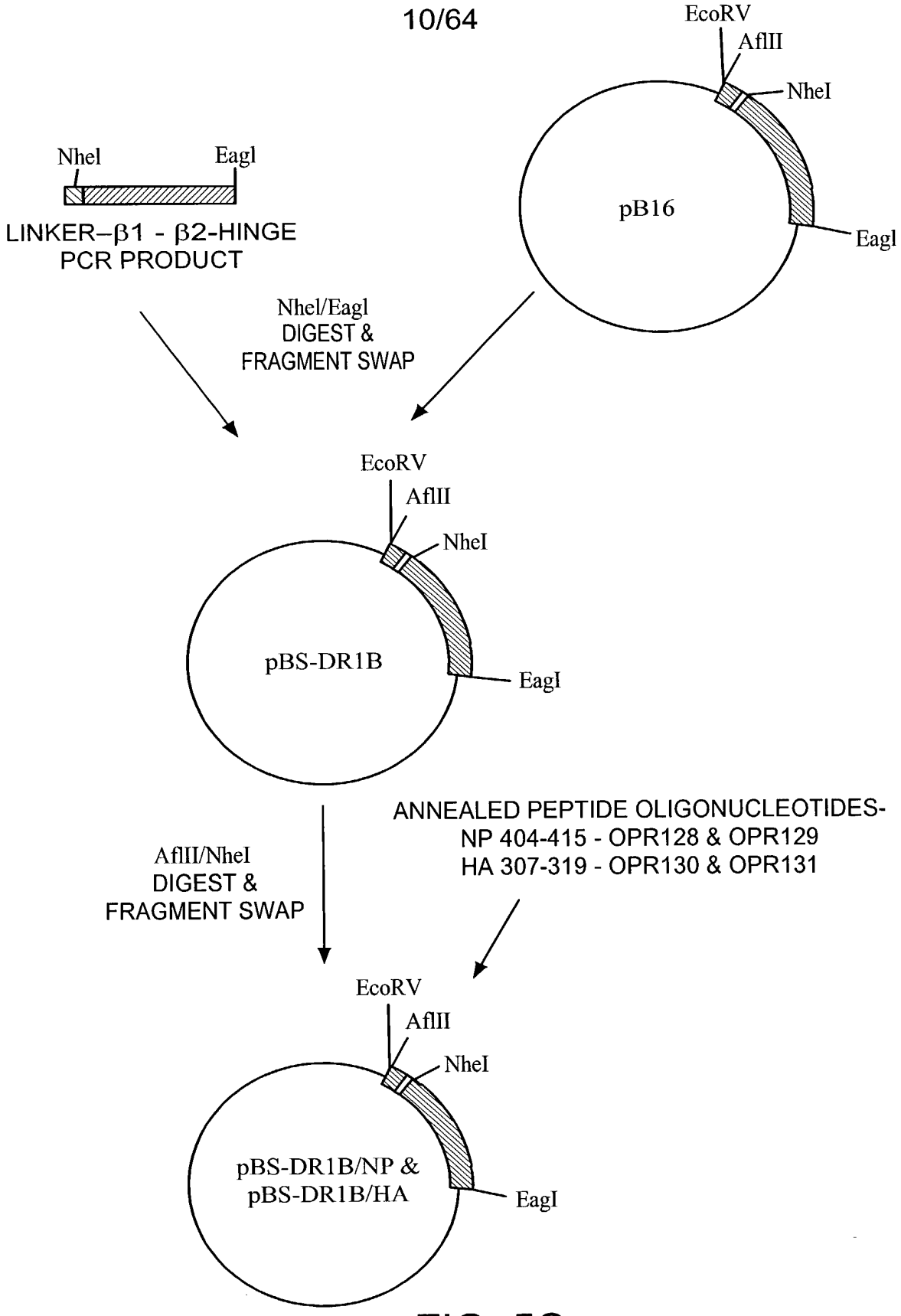
EcoRV
AflII
NheI
pB16
EagI
NheI
EagI
LINKER–β1 - β2-HINGE
PCR PRODUCT
NheI/EagI
DIGEST &
FRAGMENT SWAP
EcoRV
AflII
NheI
pBS-DR1B
EagI
ANNEALED PEPTIDE OLIGONUCLEOTIDES-
NP 404-415 - OPR128 & OPR129
HA 307-319 - OPR130 & OPR131
AflII/NheI
DIGEST &
FRAGMENT SWAP
EcoRV
AflII
NheI
pBS-DR1B/NP &
pBS-DR1B/HA
EagI

FIG. 5C

I-A^{s} α CHAIN CLONING SCHEME

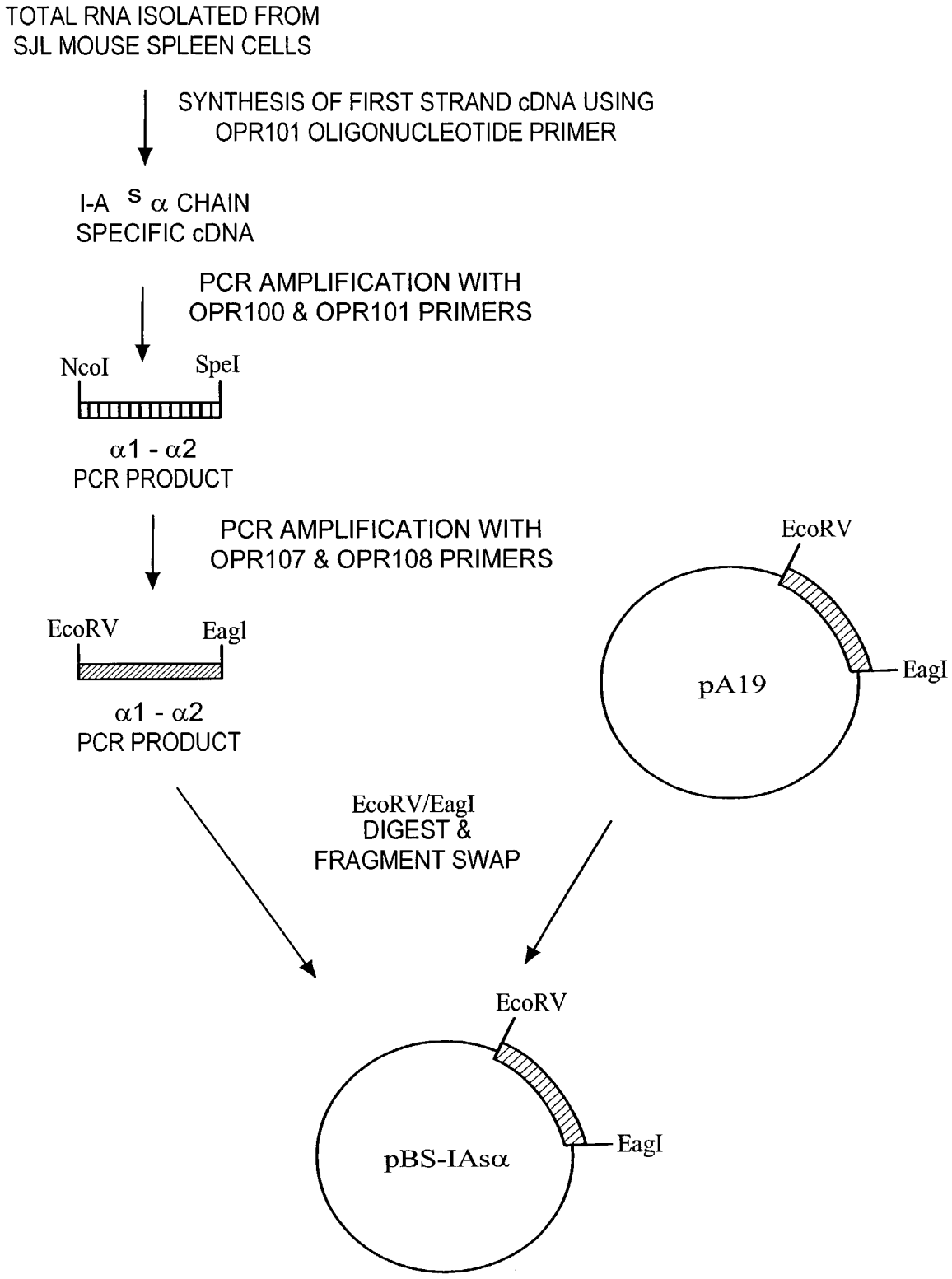

FIG. 6

FIG. 8A
FIG. 8B
FIG. 8C
FIG. 8D

FIG. 8

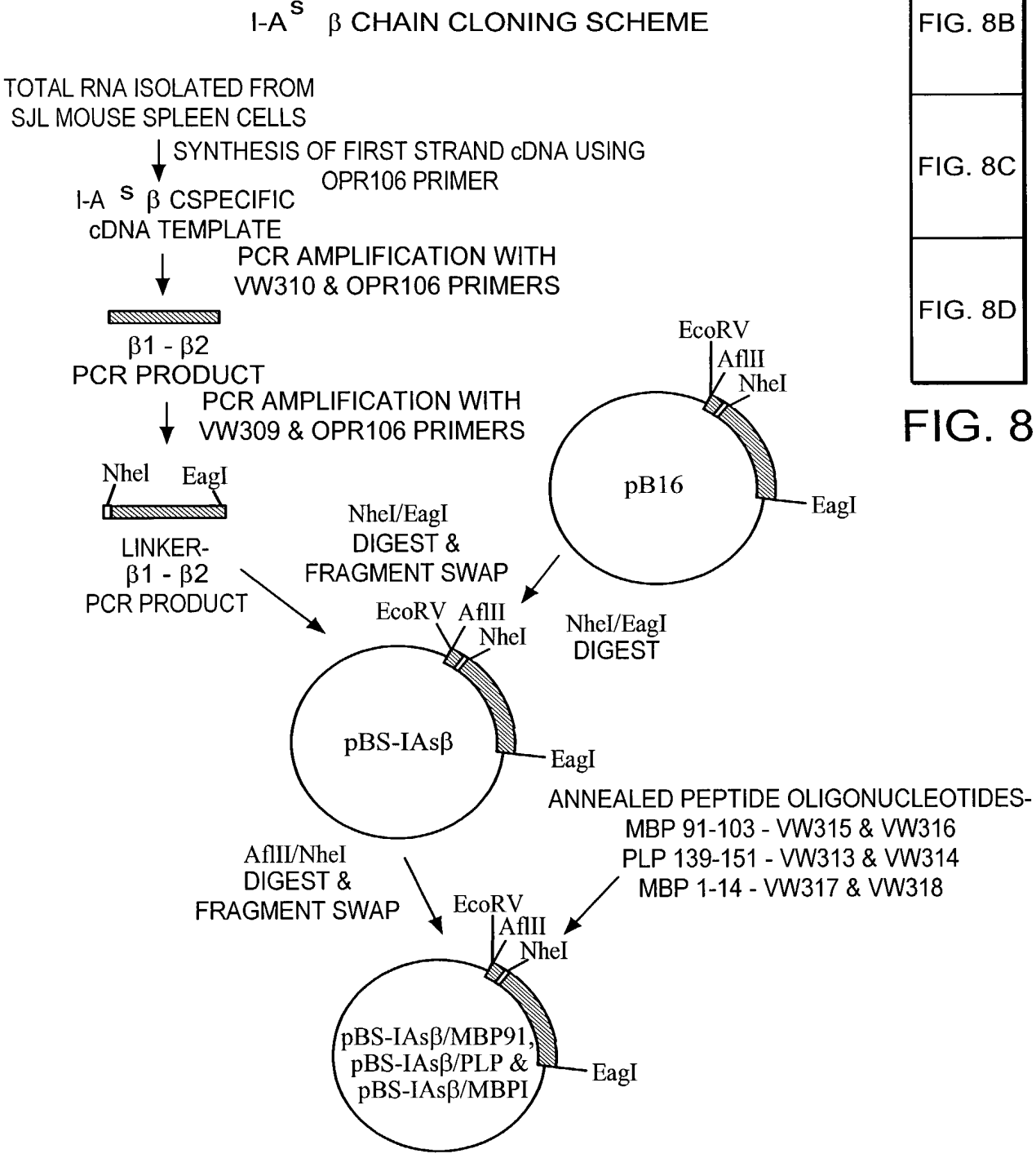

FIG. 7

OLIGOMICLEOTIDES USED IN CONSTRUCTING MHC VECTORS

I-A^d/I-A^s PCR PRIMERS AND CLONING OLIGENUCLEOTIDES (RESTRICTION SITES ARE UNDERLINED)

OPR100
5'-GGG GGG GCC ATG GCC GAA GAC GAC ATT GAG GCC GAC-3'

OPR101
5'-GGG GGG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107
5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG GCC G-3'

OPR108
5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG C-3'

OPR102
5'-GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104
5'-GCG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106
5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112
5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119
5'-AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'

OPR120-2
5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310
5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309
5'-CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136
5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC TG-3'

OPR139
5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

FIG. 8A

OPR132
5'-CCC CCC AAG CTT CCC GGG CGA CCA TGG CTC TGC AGA TCC CCA GC-3'

OPR133
5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134
5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135
5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

HLA-DR1 PCR PRIMERS AND CLONING OLIGONUCLEOTIDES

DR1A-F
5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DR1A-B
5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DR1B-F
5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG CAG C-3'

AF-N
5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S
5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124
5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA GAA GAA CAT GTG ATC-3'

OPR125
5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG AGC-3'

DR1B-B
5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN
5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA CGT TTC TTG-3'

BB-5
5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

FIG. 8B

OPR121
5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT GGT GGG GAC ACC CG-3'

OPR122
5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG GGT GTC CCC ACC ACC-3'

OPR123
5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-3'

PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339
OPR110
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT G-3'

OPR111
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA ACA GCC TGA GAG ATA C-3'

Ova H331R
OPR115
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC AAC GAA GCT GGT CGT G-3'

OPR116
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA ACA GCC TGA GAG ATA C-3'

Ova A332Y
OPR117
5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC AAC GAA GCT GGT CGT G-3'

OPR116
5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA ACA GCC TGA GAG ATA C-3'

HEL 74-86
OPR140
5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC TCC G-3'

OPR141
5'-CTA GCG GAG CTC AGC AGG GCG CTG CAGBGGG ATG TTG CAC AGG TTA C-3'

FIG. 8C

NP 404-415
OPR129
5'-TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

OPR129
5'-CTA GCC TGC ACG CTG AAG GCG GGC TEA ACG CTG ATC TGA C-3'

HA 307-319
OPR130
5'-TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC ACC G-3'

OPR131
5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG GGA C-3'

MBP 91-103
VW315
5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG CGC G-3'

VW316
5'-CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG TGA C-3'

PLP 139-151
VW313
5'-TTA CAC CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG TTC G-3'

VW314
5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG TGA C-3'

MBP 1-14
VW317
5'-TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG TAC CTG G-3'

VW316
5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT GCC ATA C-3'

FIG. 8D

SOLUBLE I-A^d α CHAIN CONSTRUCT

EcoRV ... XbaI

```
   10           20          30           40          550         560         570       580
GATATCTCAGCT TCC AGC AGT GAA GAC GAC ATT GAG GCC GAC CAC // CCG GTT CTG AAA CAC TGG AAA CGT AAGTAGCGGCCG
CTATAGAGTCGA AGG TCG TCA CTT CTG CTG TAA CTC CGG CTG GTG // GGC CAA GAC TTT GTG ACC TTT GCA TTCATCGCCGGC
              S   S   S   E   D   D   I   E   A   D   H // P   V   L   K   H   W   K   R
```

-1 ... aa192

IgG < CHAIN INTRON

SIGNAL PEPTIDE CLEAVAGE SITE

I-A$^\alpha$ α CHAIN

IgG < CHAIN INTRON

FIG. 9A

SOLUBLE I-A^d β CHAIN CONSTRUCT

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

EcoRV

AflII NheI

```
   10           20          30          40          50          60          70
GATATCACAGGT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT //
CTATAGTGTCCA CAG AAT TCA CCT CGA TCG CCT CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA //
              V   L   S ↑ G   A   S   G   G   G   G   S   G   G   G   G   N   S   E   R   H  //
```

+1

IgG H CHAIN INTRON

SIGNAL PEPTIDE CLEAVAGE SITE

LINKER REGION

I-A$^\alpha$ β CHAIN

XbaI

```
610         620         630
ATC ACT GTG GAG TGG TCC TCA GGT ACGGCCGCC
TAG TGA CAC CTC ACC AGG AGT CCA TGCCGGCGG
 L   T   V   E   W   S   S
```

aaL89

I-A$^\alpha$ β CHAIN

IgG H CHAIN INTRON

FIG. 9B

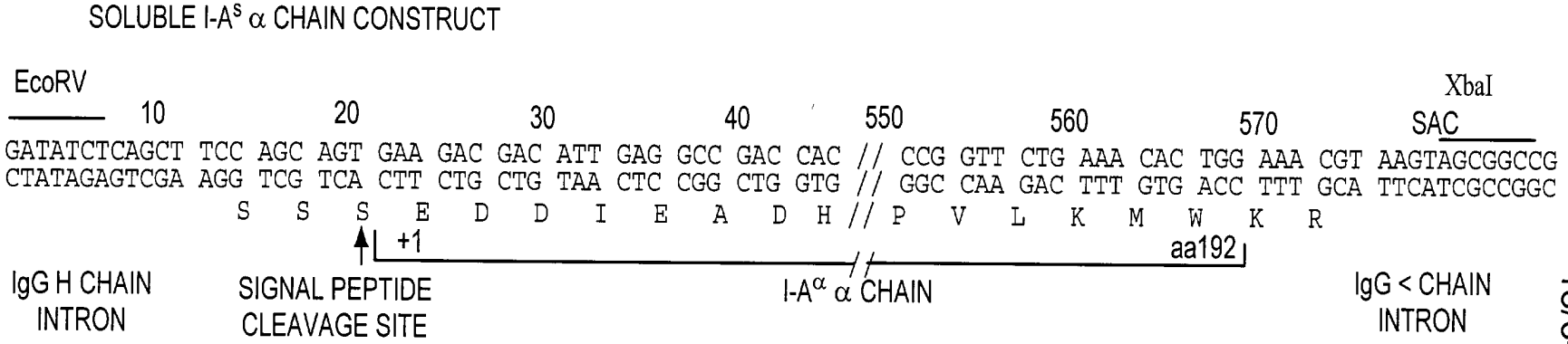

FIG. 9C

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

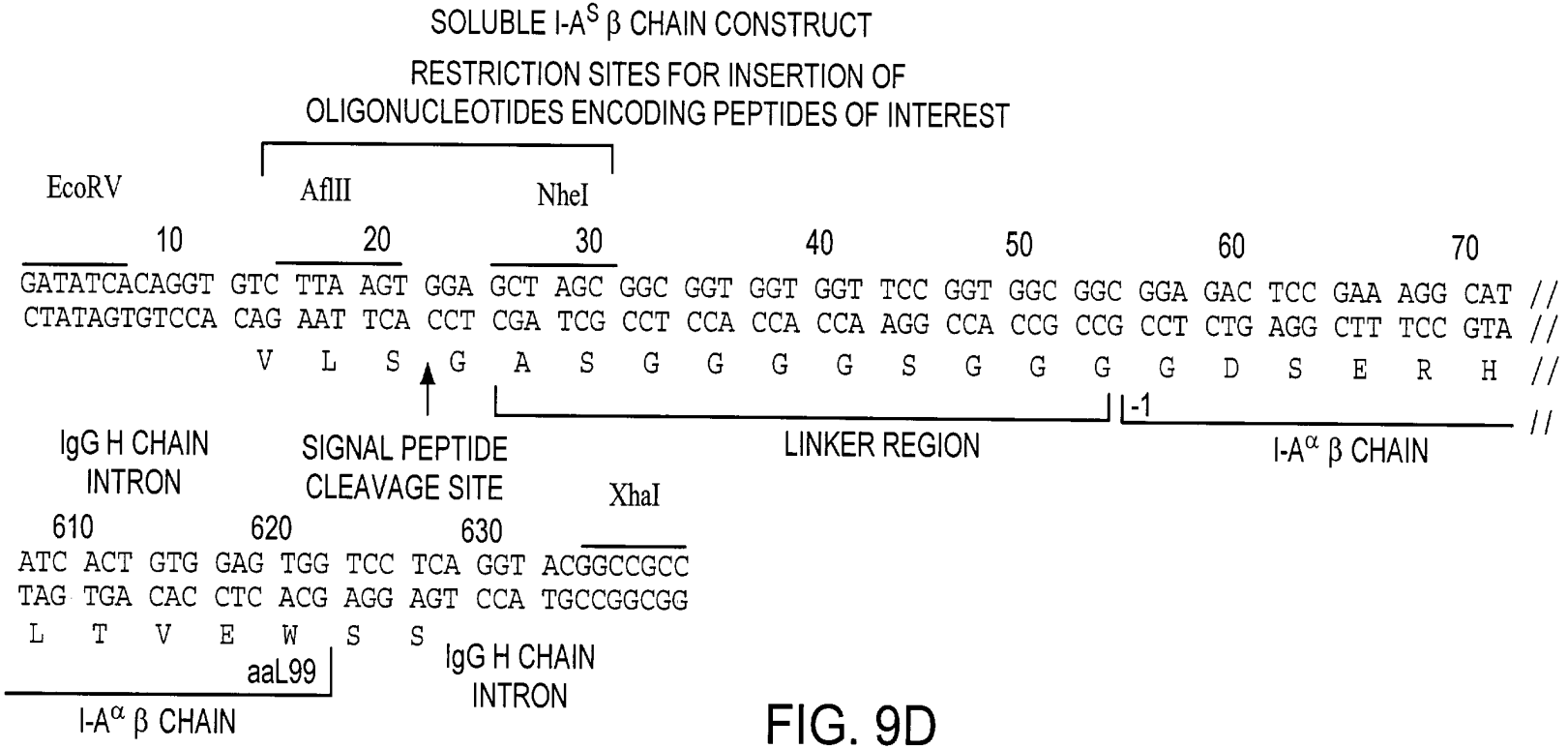

FIG. 9D

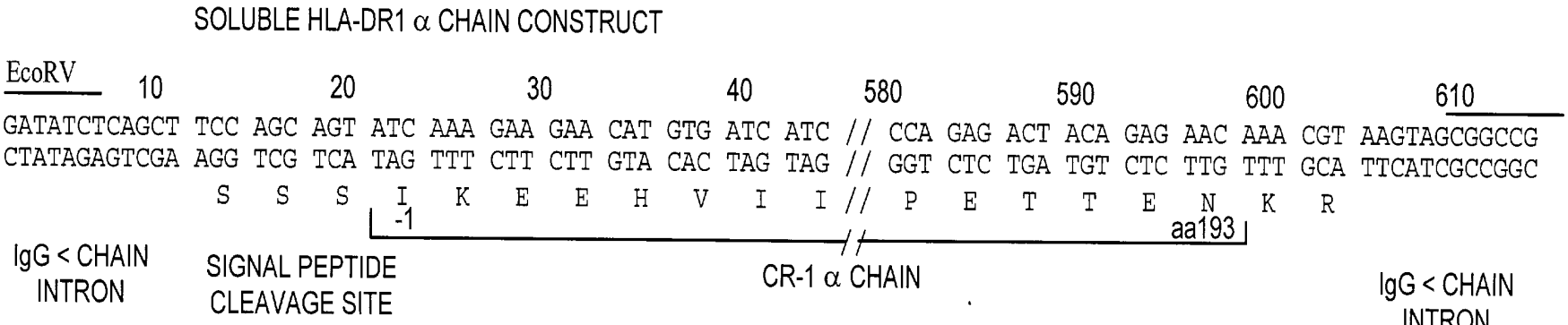

FIG. 9E

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

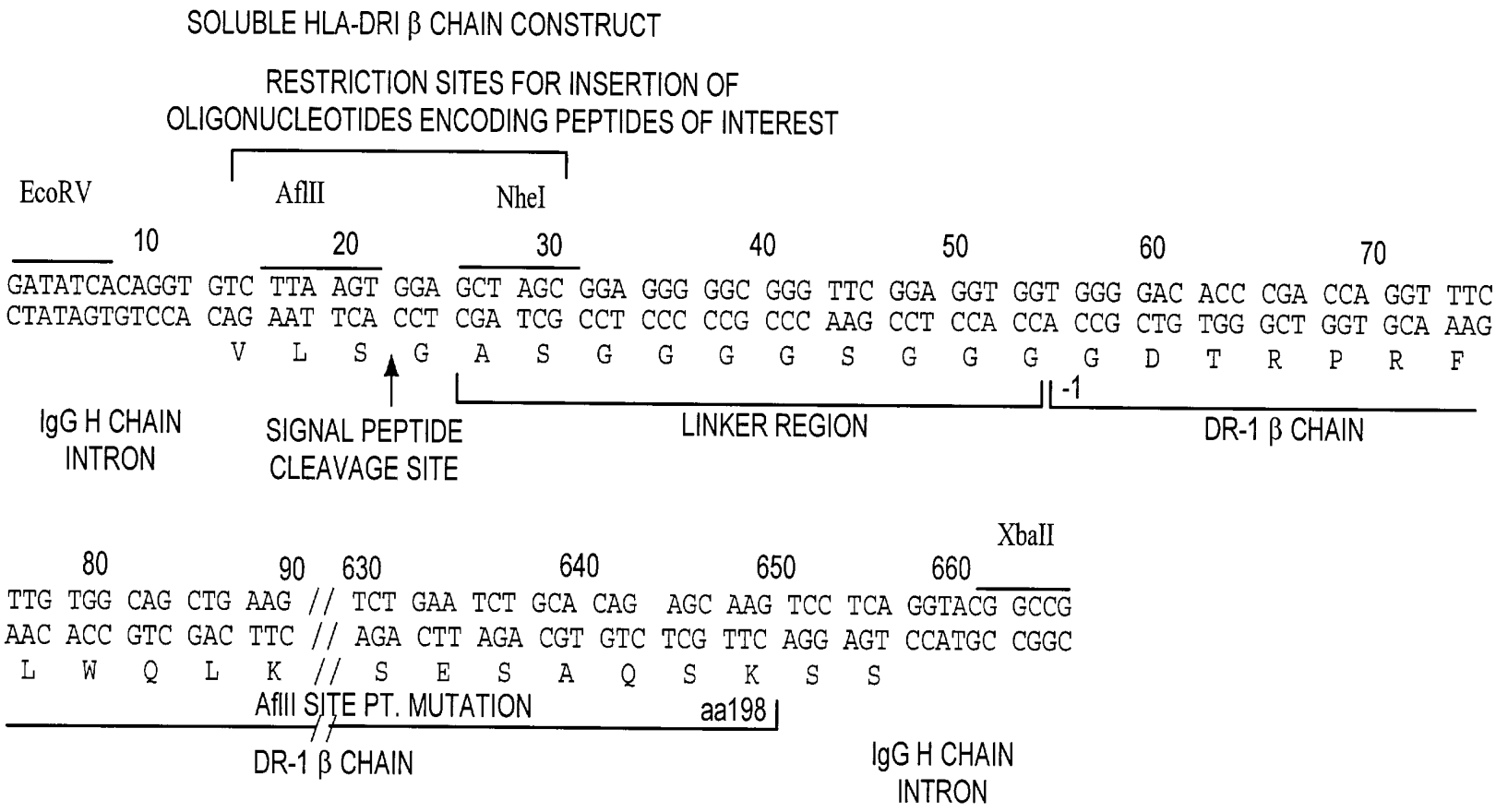

FIG. 9F

ORIGINAL MAMMALIAN CELL EXPRESSION VECTORS

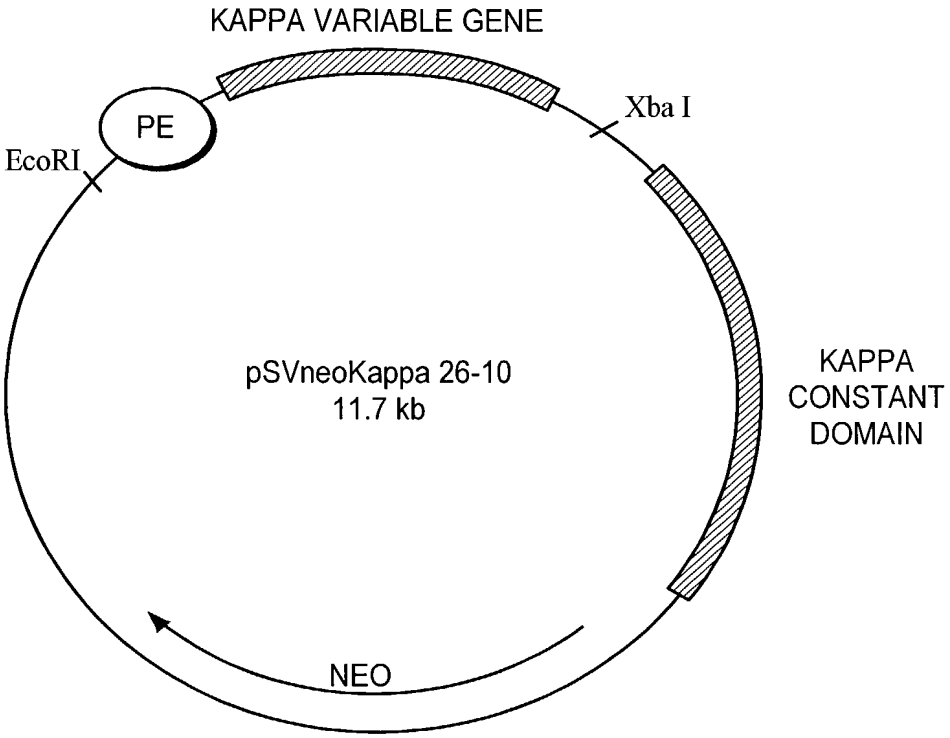

FIG. 10A

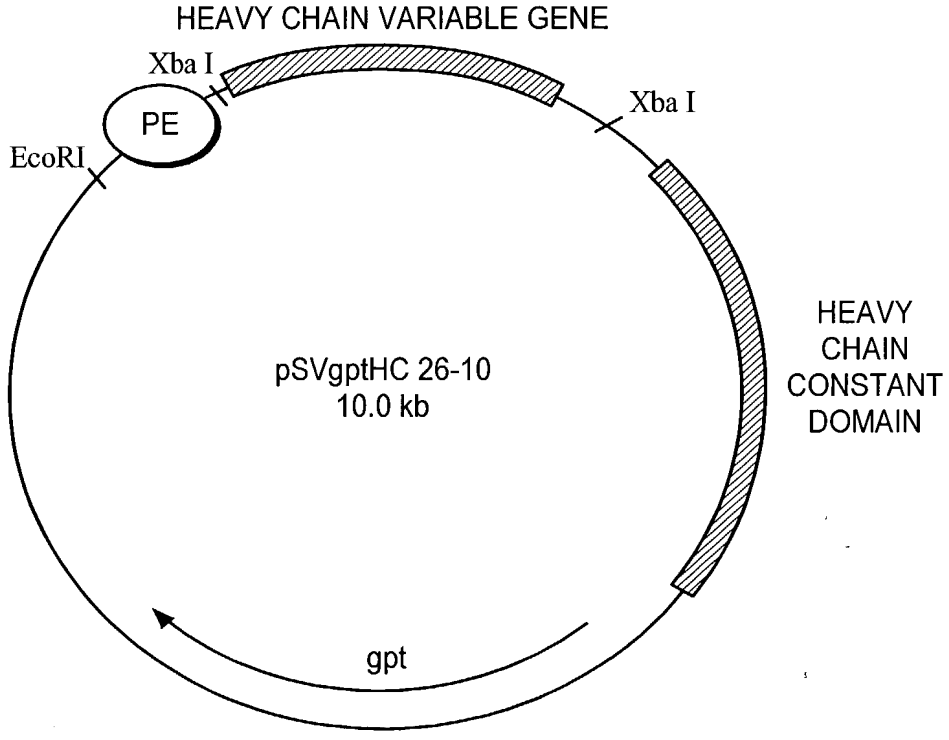

FIG. 10B

THE 2.7 Kb KAPPA AND THE 1.7 Kb HEAVY CHAIN EcoR V AND Eag I. MUTATED CONSTRUCTS

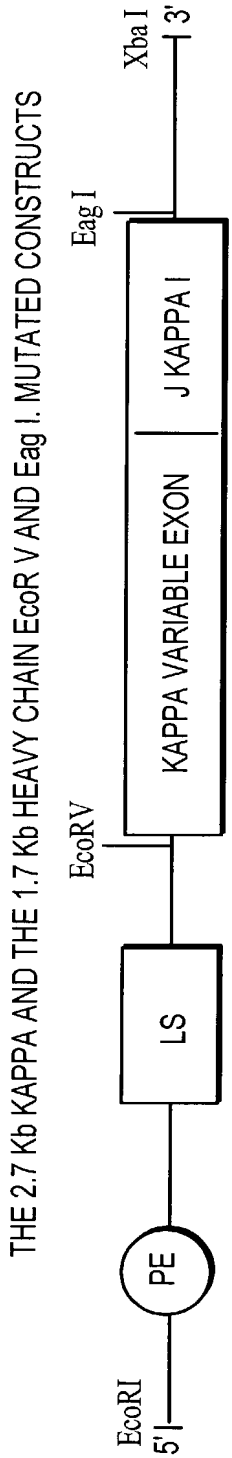

FIG. 11A

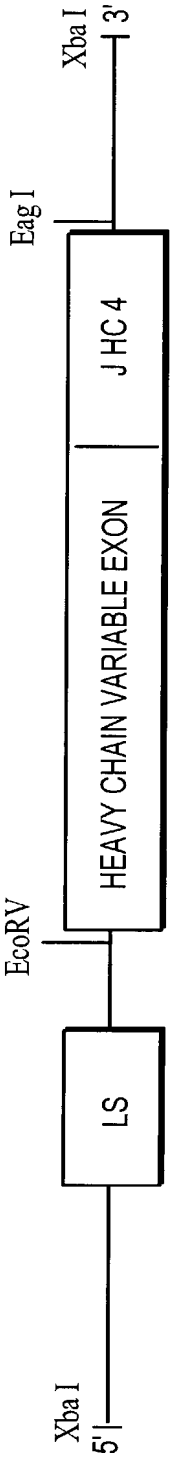

FIG. 11B

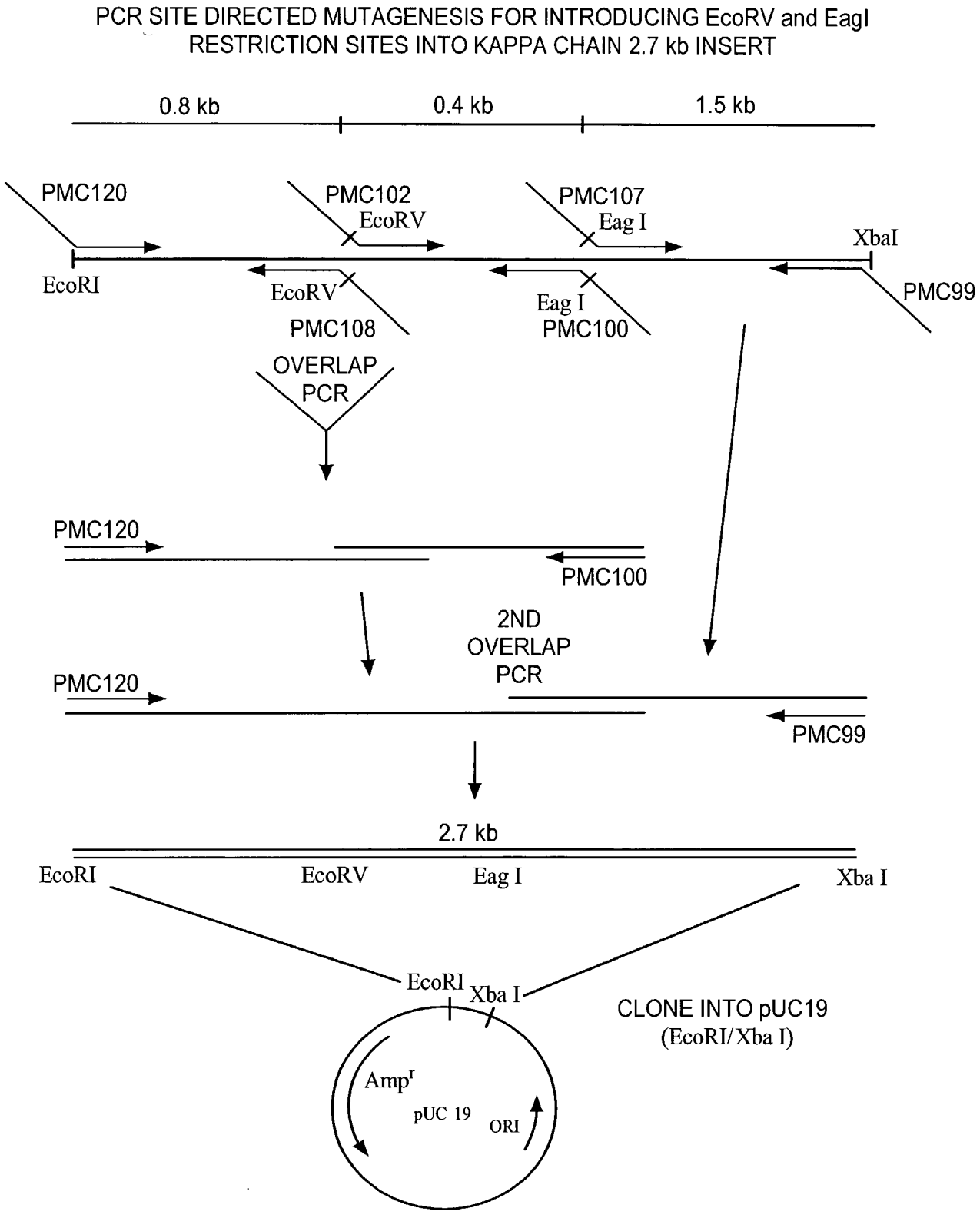
PCR SITE DIRECTED MUTAGENESIS FOR INTRODUCING EcoRV and EagI RESTRICTION SITES INTO KAPPA CHAIN 2.7 kb INSERT
0.8 kb
0.4 kb
1.5 kb
PMC120
PMC102
EcoRV
PMC107
Eag I
XbaI
EcoRI
EcoRV
PMC108
Eag I
PMC100
PMC99
OVERLAP
PCR
PMC120
PMC100
2ND
OVERLAP
PCR
PMC120
PMC99
2.7 kb
EcoRI
EcoRV
Eag I
Xba I
EcoRI
Xba I
CLONE INTO pUC19
(EcoRI/Xba I)
Amp^r
pUC 19
ORI

FIG. 12

STRATEGY FOR CONSTRUCTING MHC CLASS IIc/KAPPA CONSTANT GENE IN MAMMALIAN CELL EXPRESSION VECTOR

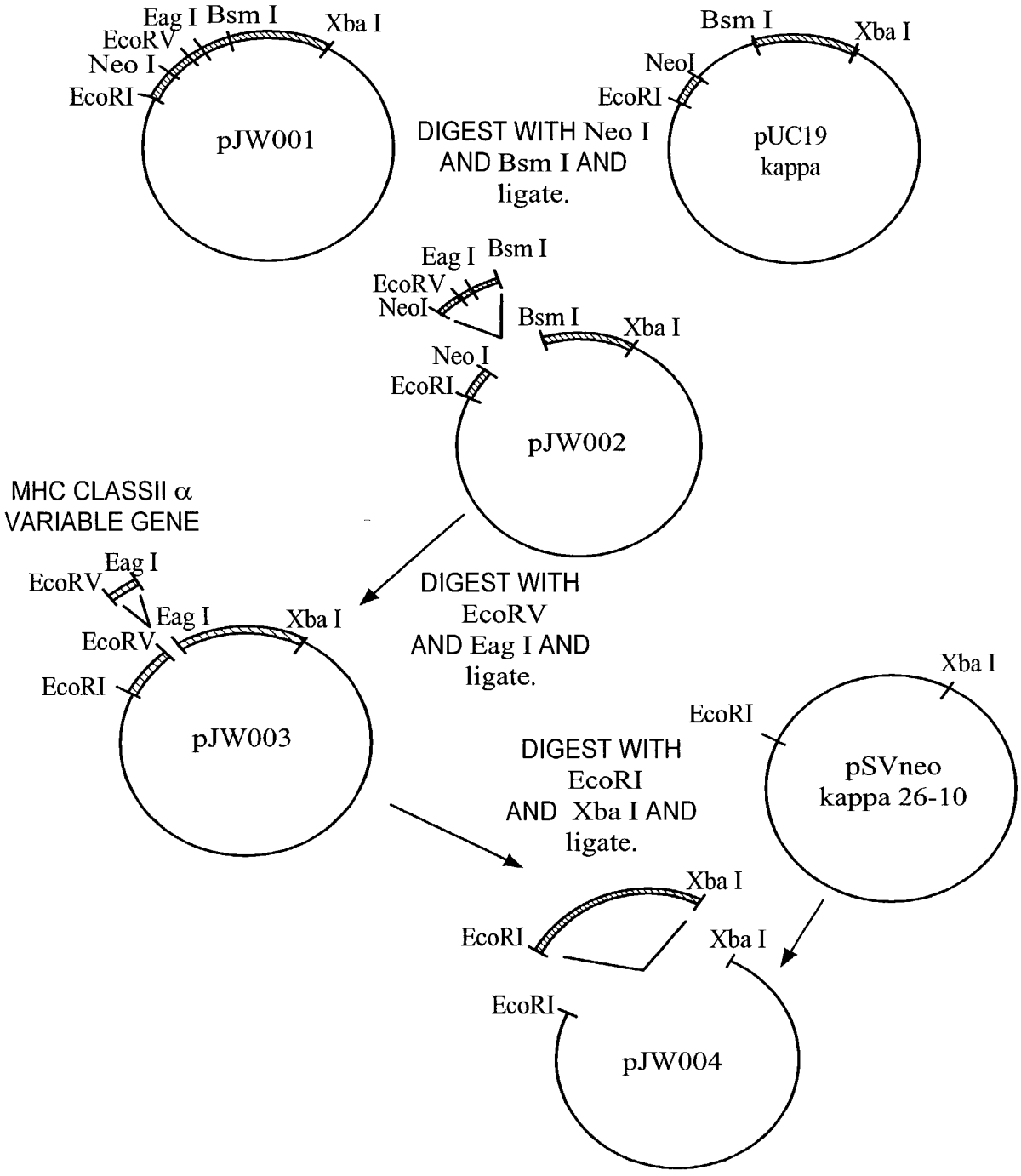

FIG. 13

PRIMERS USED FOR SEQUENCING MUTATED 2.7Kb FRAGMENT

PRIMER LIST	SEQUENCE
PMC-33	(5'GCTCAGCTGTCTTGTTTCAGTACTGATC3')
PMC-77	(5'GTAAGTAGCGGCCG3')
PMC-111	(5'GGTATGTAAAAATAAACATCACAG3')
PMC-114	(5'GCTTTGCTTACGGAGTTACTC3')

FIG. 14

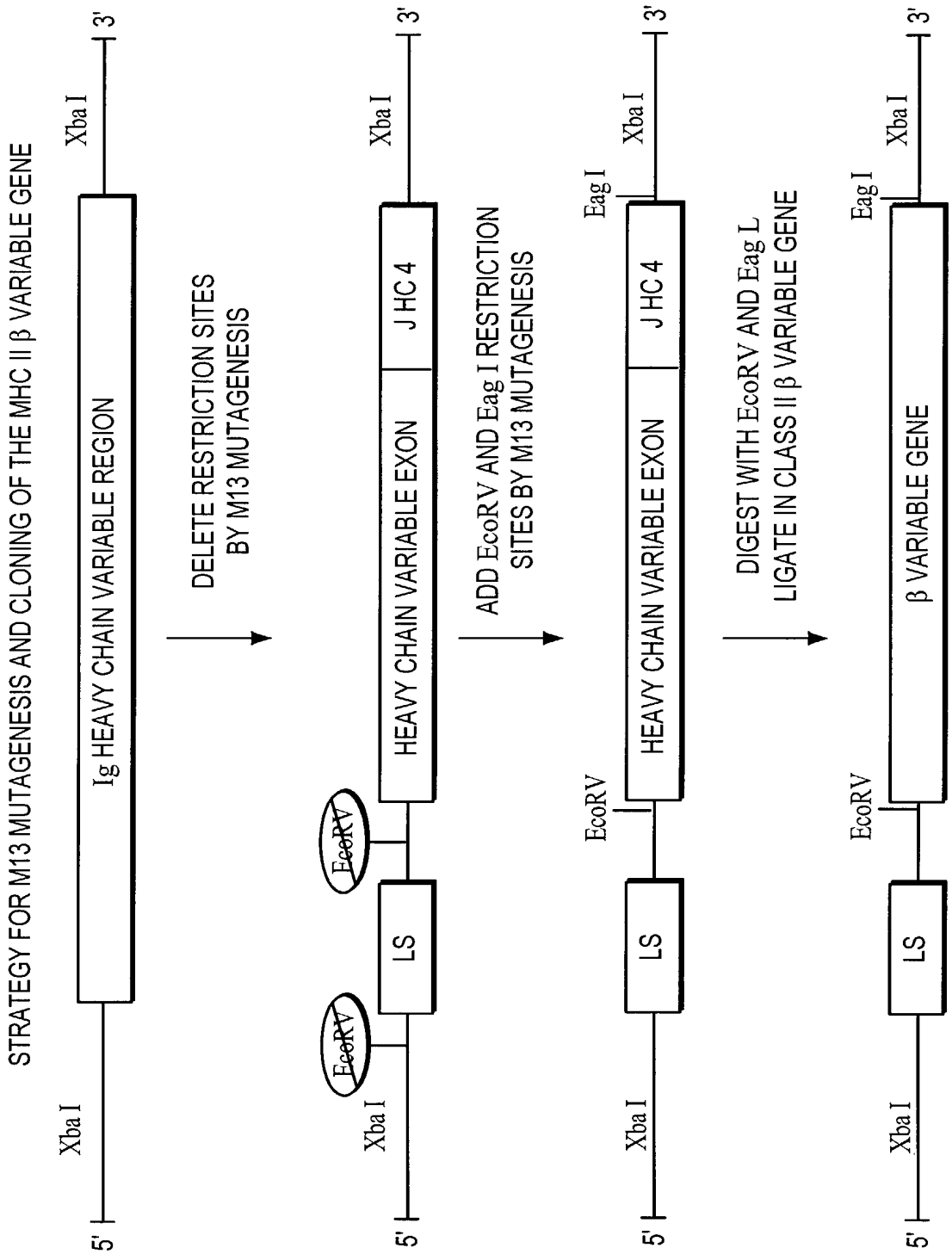
STRATEGY FOR M13 MUTAGENESIS AND CLONING OF THE MHC II β VARIABLE GENE
Xba I
3'
Ig HEAVY CHAIN VARIABLE REGION
Xba I
5'
DELETE RESTRICTION SITES
BY M13 MUTAGENESIS
Xba I
3'
HEAVY CHAIN VARIABLE EXON
J HC 4
EcoRV
LS
EcoRV
Xba I
5'
ADD EcoRV AND Eag I RESTRICTION
SITES BY M13 MUTAGENESIS
Eag I
Xba I
3'
HEAVY CHAIN VARIABLE EXON
J HC 4
EcoRV
LS
Xba I
5'
DIGEST WITH EcoRV AND Eag L
LIGATE IN CLASS II β VARIABLE GENE
Eag I
Xba I
3'
β VARIABLE GENE
EcoRV
LS
Xba I
5'

FIG. 15

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

FINAL VECTORS FOR EXPRESSING MHC II/Ig CHIMERIC PROTEINS

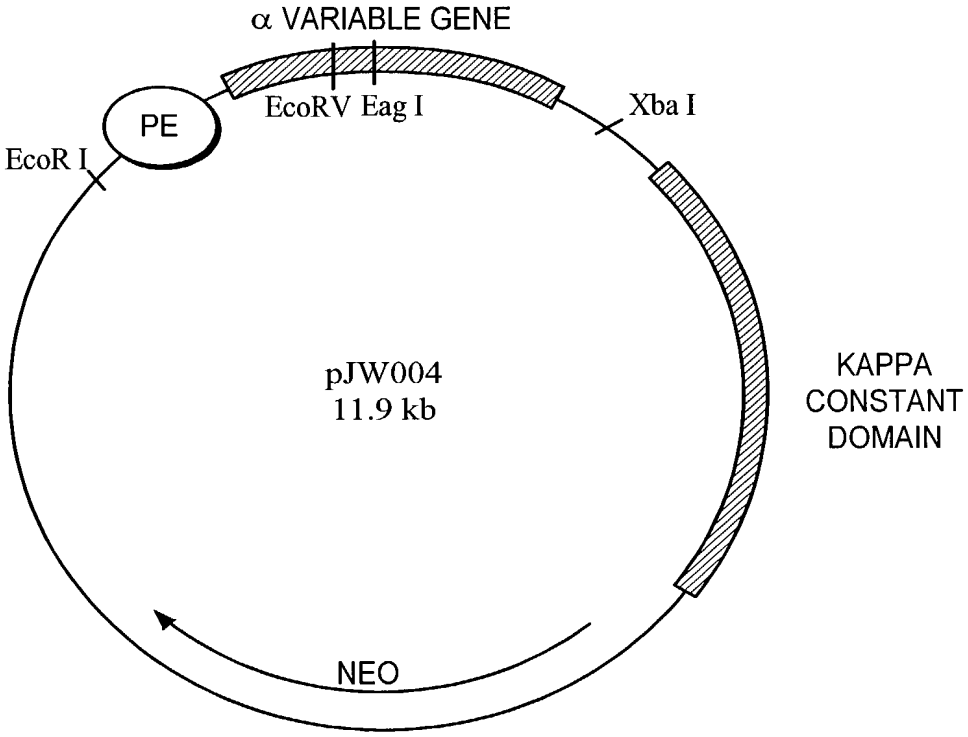

FIG. 16A

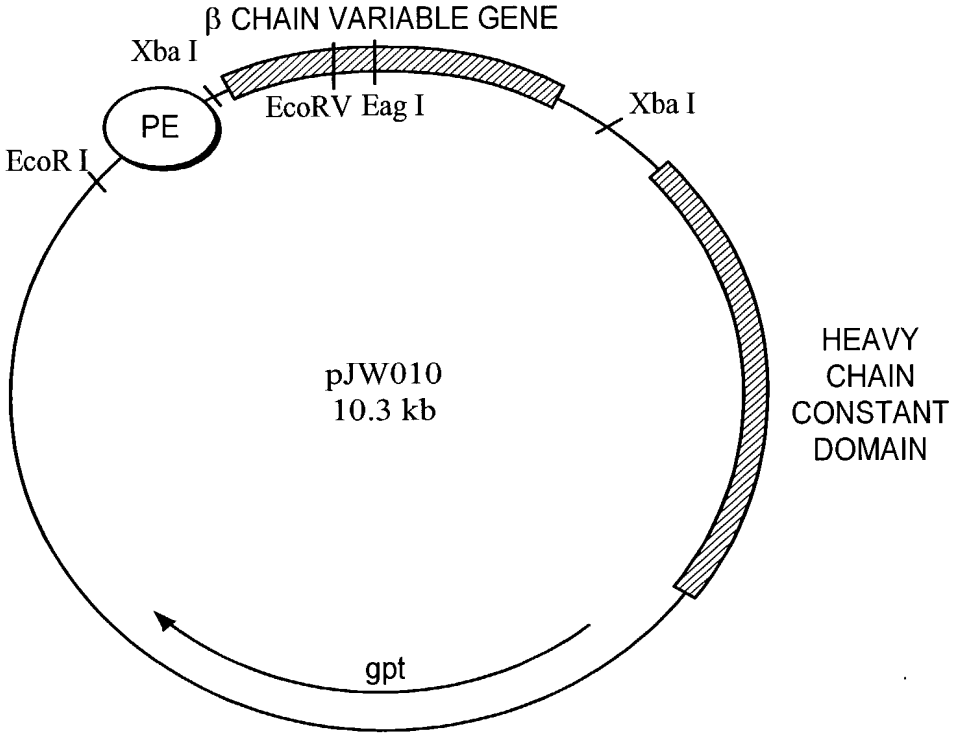

FIG. 16B

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

FIG. 17A
FIG. 17B
FIG. 17C

FIG. 17

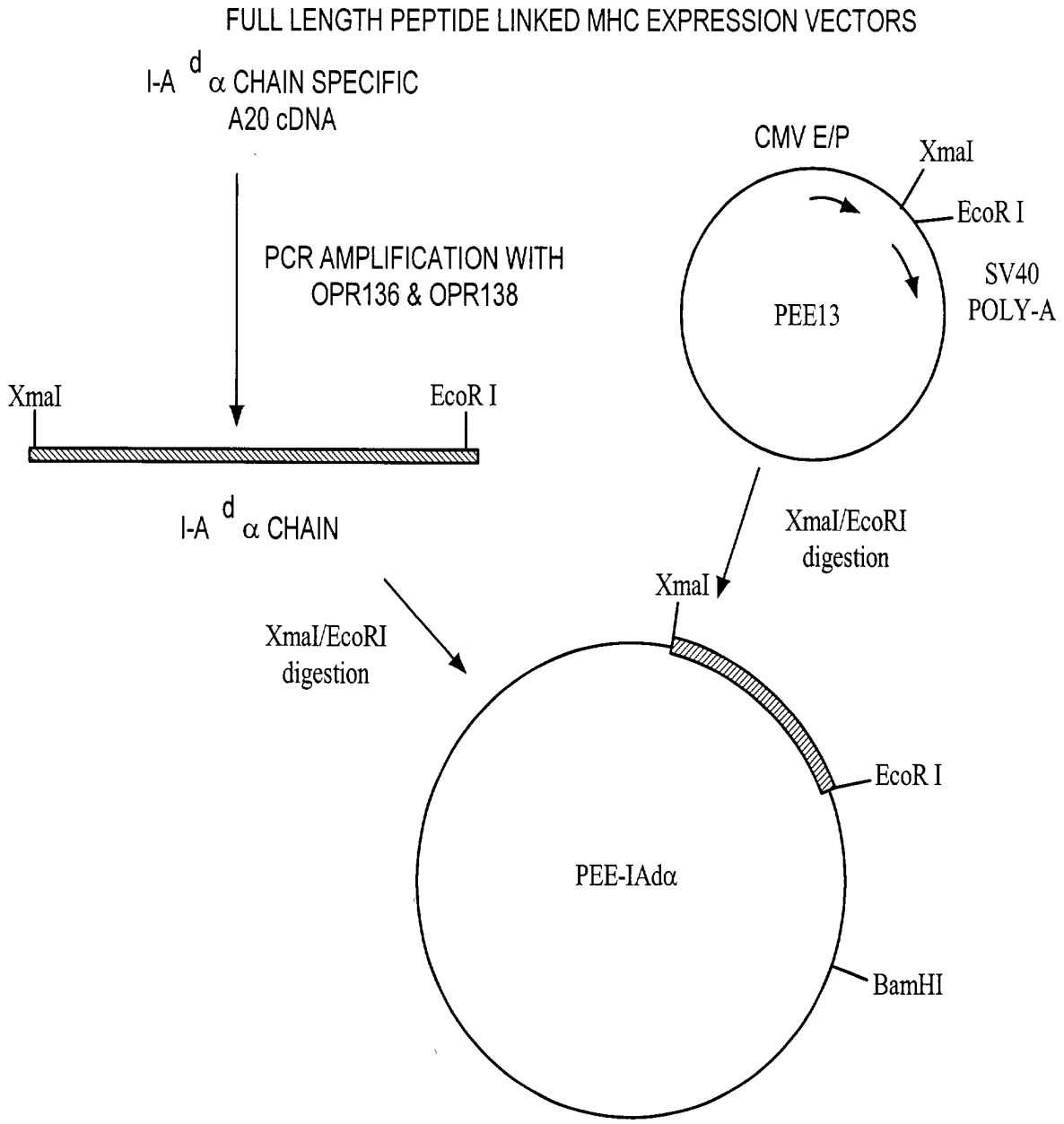

FIG. 17A

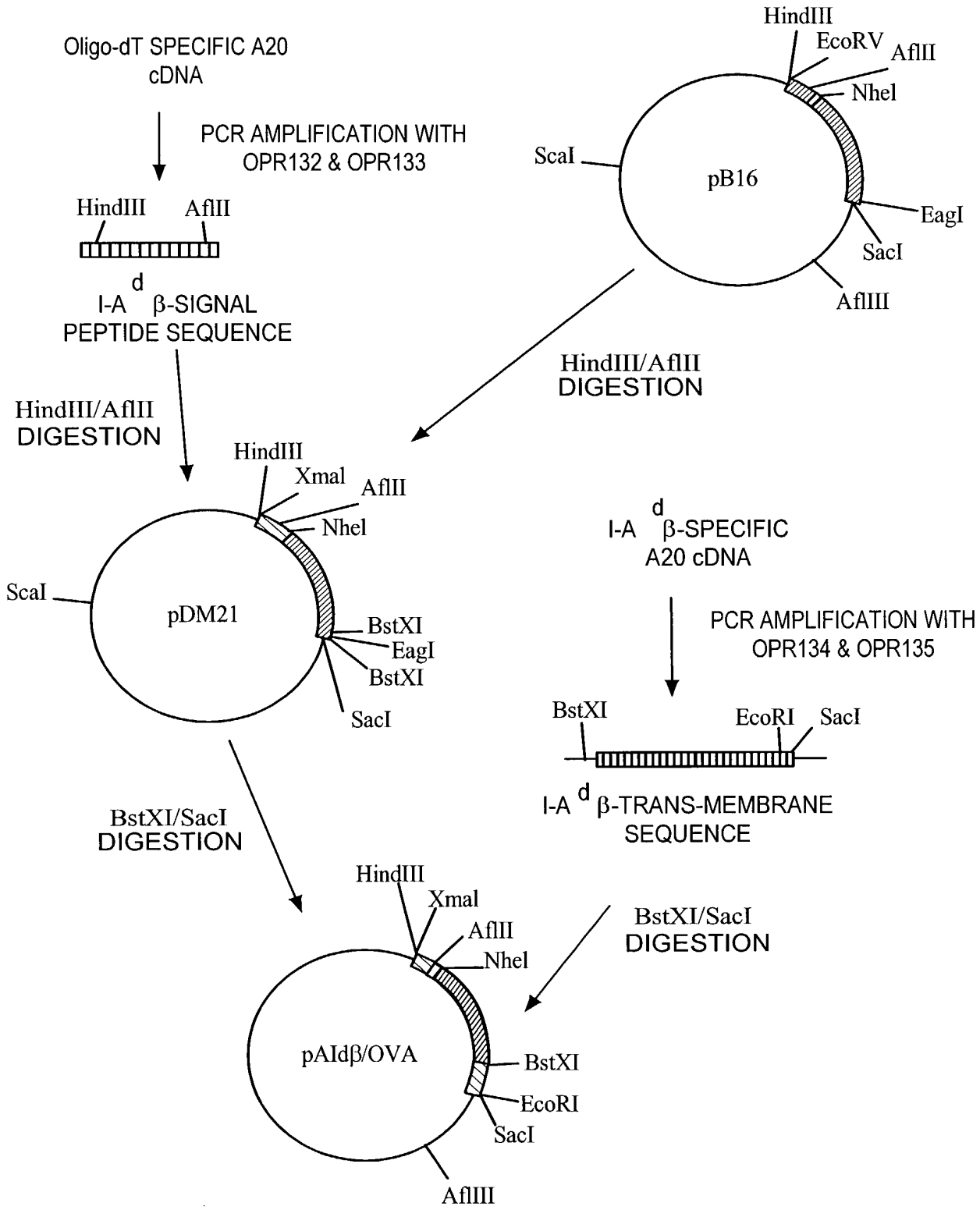
Oligo-dT SPECIFIC A20 cDNA
PCR AMPLIFICATION WITH OPR132 & OPR133
HindIII
AflII
d
I-A β-SIGNAL PEPTIDE SEQUENCE
HindIII/AflII DIGESTION
HindIII
EcoRV
AflII
NheI
ScaI
pB16
EagI
SacI
AflIII
HindIII/AflII DIGESTION
HindIII
XmaI
AflII
NheI
ScaI
pDM21
BstXI
EagI
BstXI
SacI
d
I-A β-SPECIFIC A20 cDNA
PCR AMPLIFICATION WITH OPR134 & OPR135
BstXI
EcoRI
SacI
I-A d β-TRANS-MEMBRANE SEQUENCE
BstXI/SacI DIGESTION
BstXI/SacI DIGESTION
HindIII
XmaI
AflII
NheI
pAIdβ/OVA
BstXI
EcoRI
SacI
AflIII

FIG. 17B

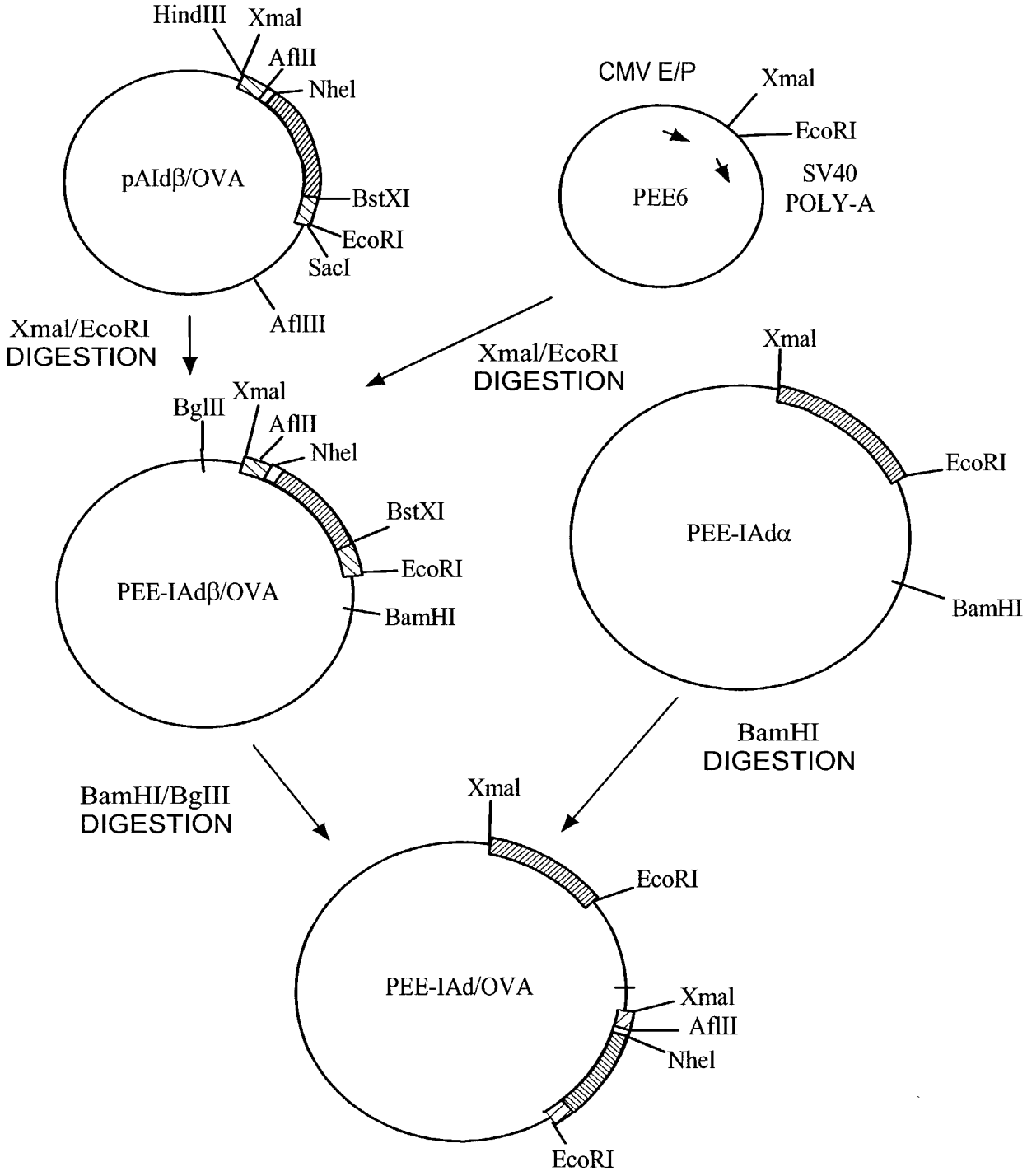
HindIII
XmaI
AflII
NheI
pAIdβ/OVA
BstXI
EcoRI
SacI
AflIII
CMV E/P
XmaI
EcoRI
PEE6
SV40
POLY-A
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
BglII
XmaI
AflII
NheI
BstXI
EcoRI
PEE-IAdβ/OVA
BamHI
XmaI
EcoRI
PEE-IAdα
BamHI
BamHI
DIGESTION
BamHI/BgIII
DIGESTION
XmaI
EcoRI
PEE-IAd/OVA
XmaI
AflII
NheI
EcoRI

FIG. 17C

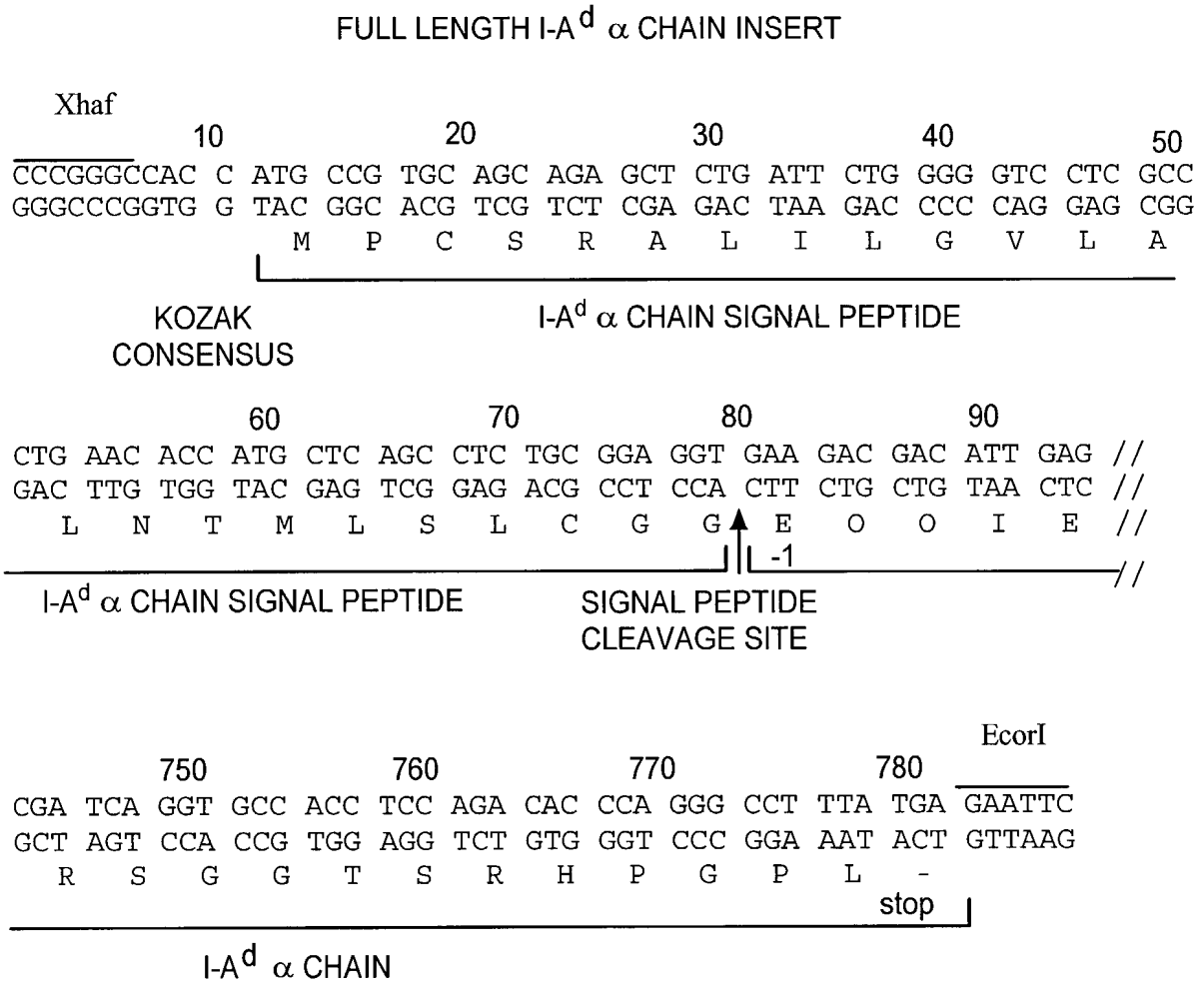
FULL LENGTH I-A^d α CHAIN INSERT
Xhaf
10 20 30 40 50
CCCGGGCCAC C ATG CCG TGC AGC AGA GCT CTG ATT CTG GGG GTC CTC GCC
GGGCCCGGTG G TAC GGC ACG TCG TCT CGA GAC TAA GAC CCC CAG GAG CGG
M P C S R A L I L G V L A
KOZAK CONSENSUS
I-A^d α CHAIN SIGNAL PEPTIDE
60 70 80 90
CTG AAC ACC ATG CTC AGC CTC TGC GGA GGT GAA GAC GAC ATT GAG //
GAC TTG TGG TAC GAG TCG GAG ACG CCT CCA CTT CTG CTG TAA CTC //
L N T M L S L C G G E O O I E //
-1
I-A^d α CHAIN SIGNAL PEPTIDE
SIGNAL PEPTIDE CLEAVAGE SITE
EcorI
750 760 770 780
CGA TCA GGT GCC ACC TCC AGA CAC CCA GGG CCT TTA TGA GAATTC
GCT AGT CCA CCG TGG AGG TCT GTG GGT CCC GGA AAT ACT GTTAAG
R S G G T S R H P G P L -
stop
I-A^d α CHAIN

FIG. 18A

FULL LENGTH I-A^d β CHAIN INSERT

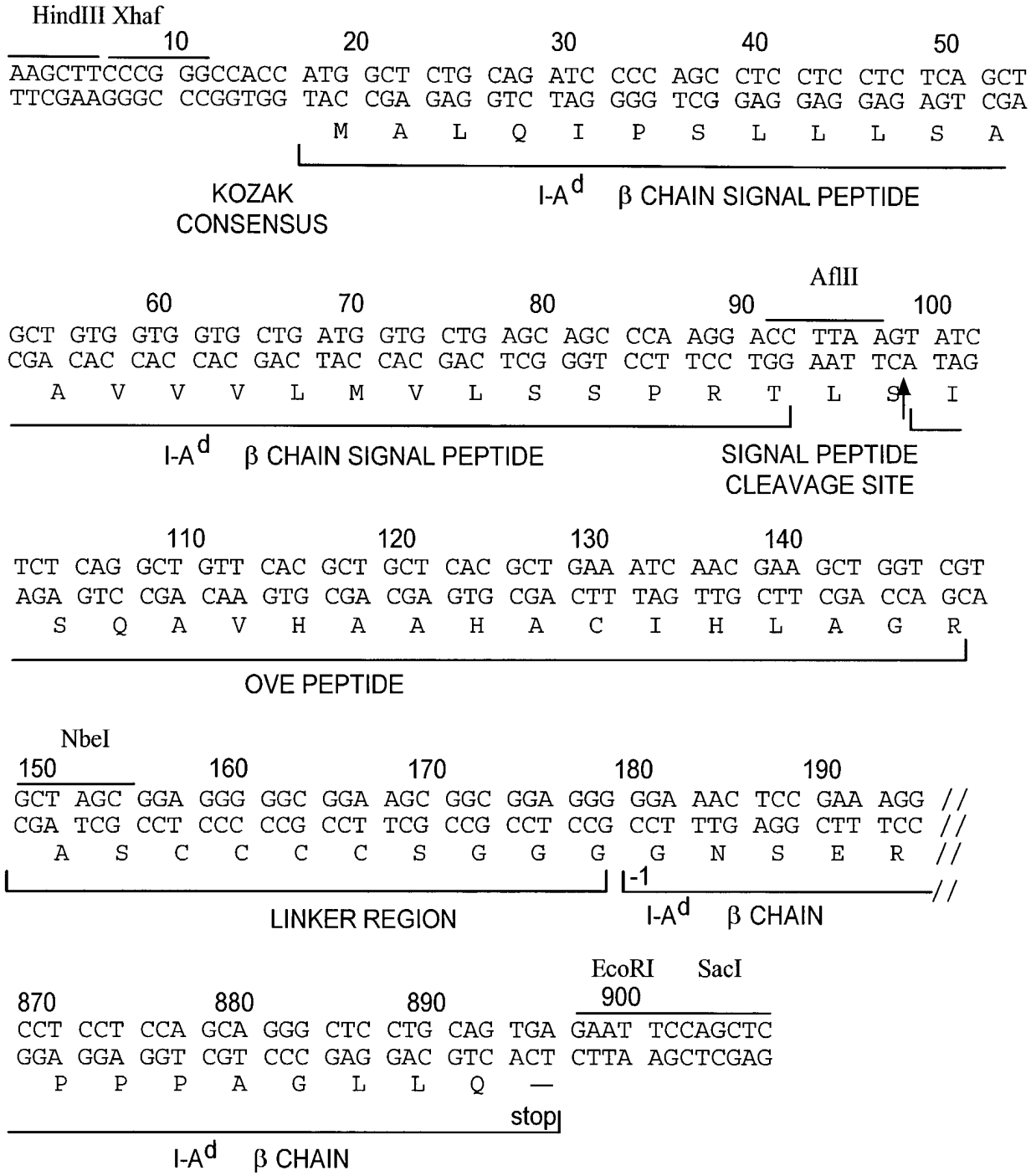

FIG. 18B

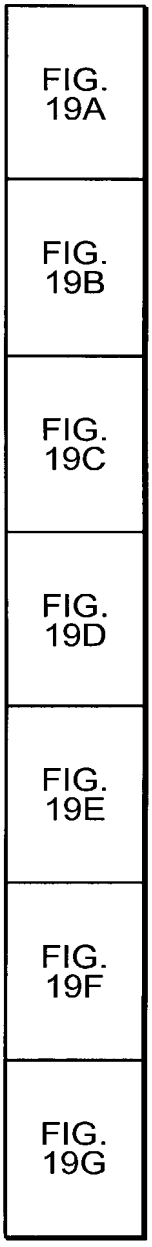

FIG. 19

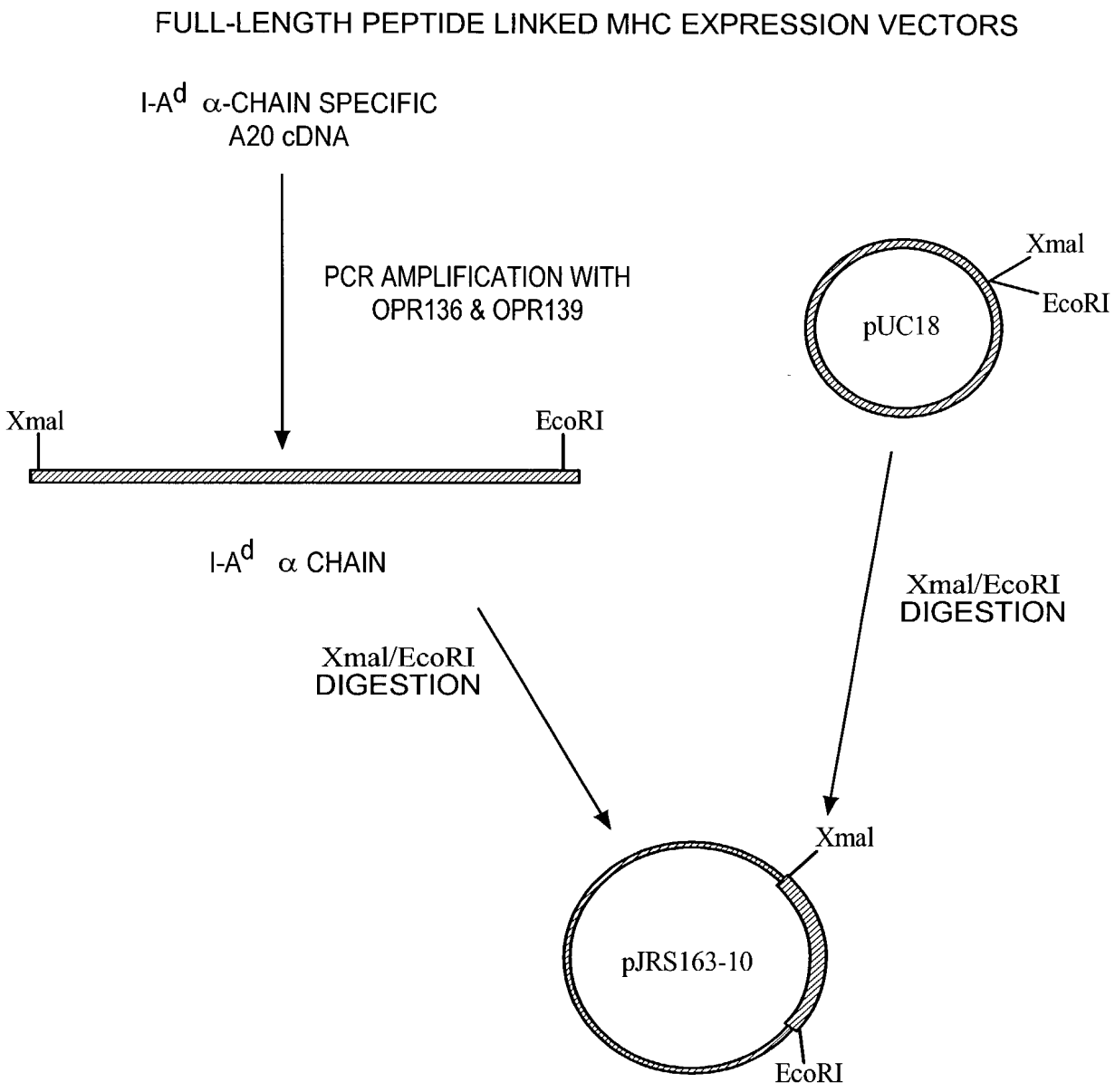
FULL-LENGTH PEPTIDE LINKED MHC EXPRESSION VECTORS
I-A^d α-CHAIN SPECIFIC
A20 cDNA
PCR AMPLIFICATION WITH
OPR136 & OPR139
XmaI
EcoRI
I-A^d α CHAIN
pUC18
XmaI
EcoRI
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
pJRS163-10
XmaI
EcoRI

FIG. 19A

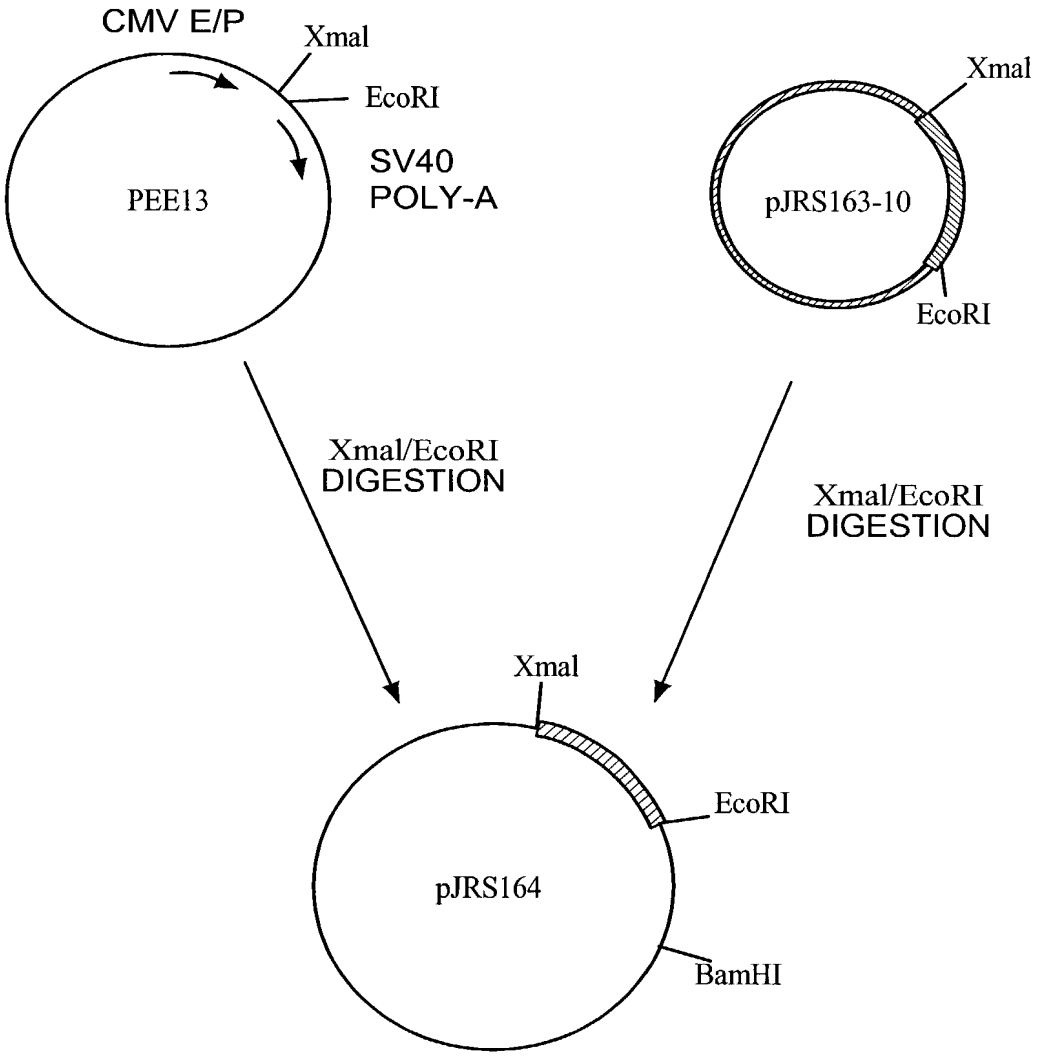
CMV E/P
XmaI
EcoRI
SV40
POLY-A
PEE13
XmaI
pJRS163-10
EcoRI
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
XmaI
EcoRI
pJRS164
BamHI

FIG. 19B

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

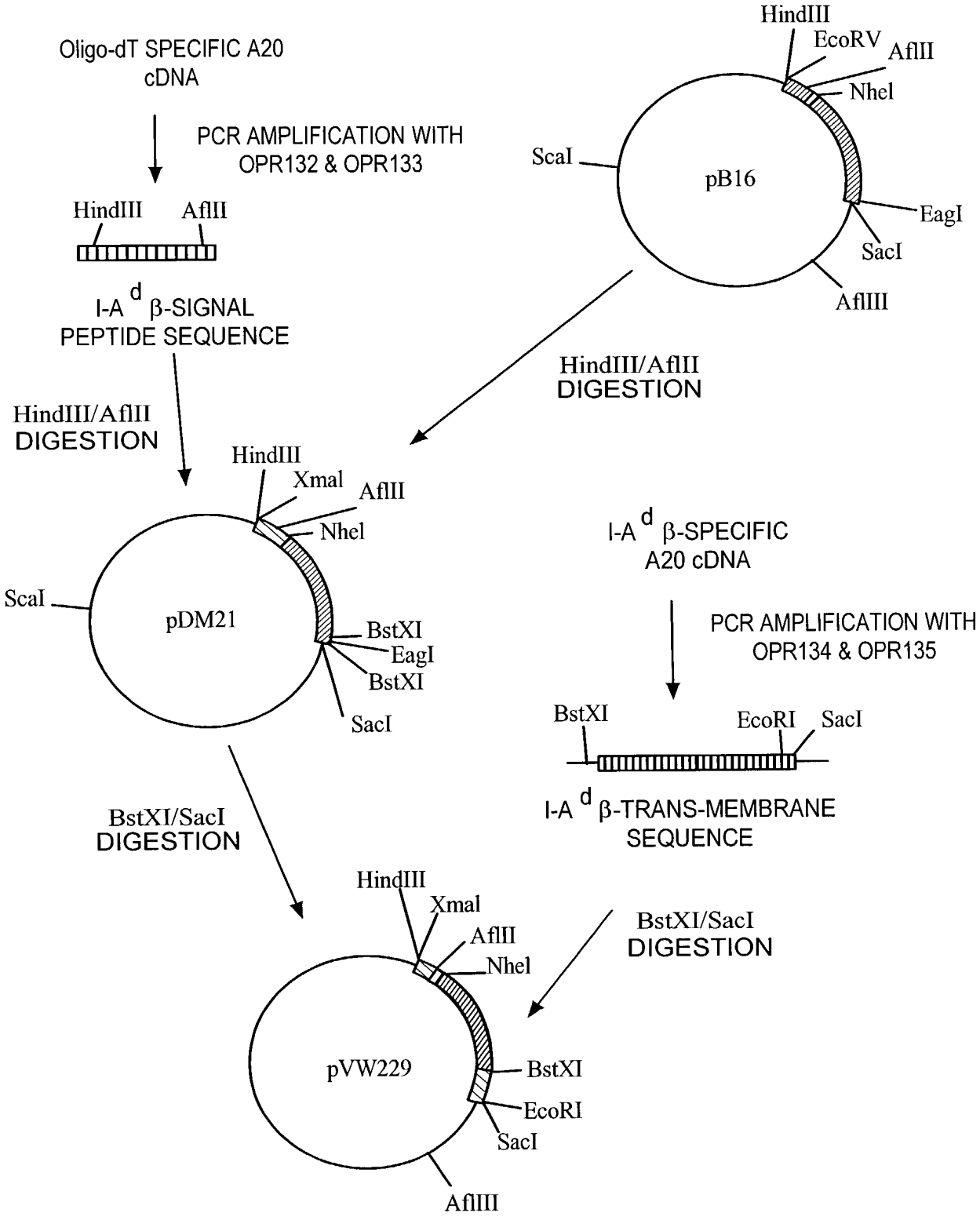

FIG. 19C

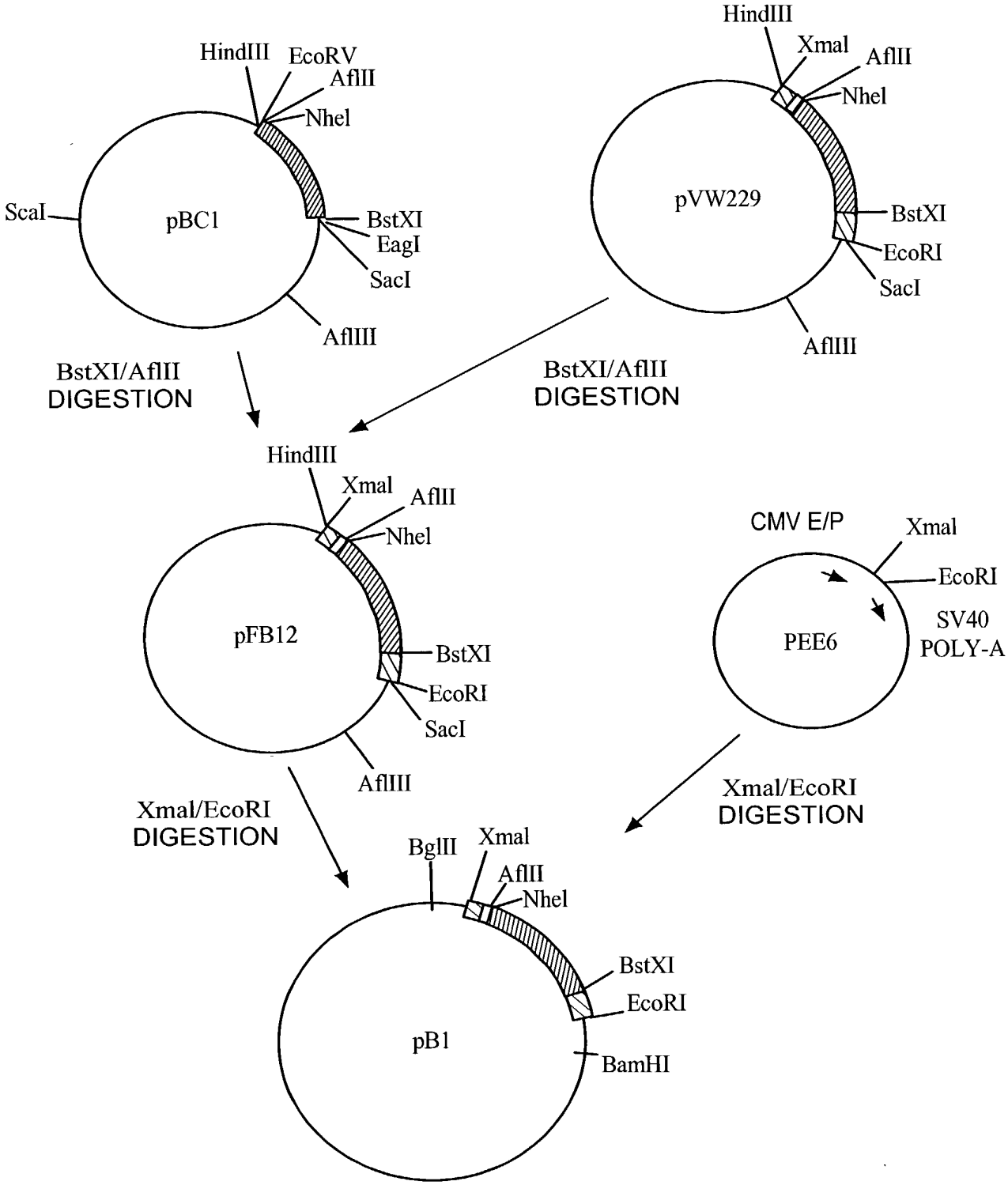
HindIII
EcoRV
AflII
NheI
ScaI
pBC1
BstXI
EagI
SacI
AflIII
BstXI/AflII
DIGESTION
HindIII
XmaI
AflII
NheI
pVW229
BstXI
EcoRI
SacI
AflIII
BstXI/AflII
DIGESTION
HindIII
XmaI
AflII
NheI
pFB12
BstXI
EcoRI
SacI
AflIII
XmaI/EcoRI
DIGESTION
CMV E/P
XmaI
EcoRI
SV40
POLY-A
PEE6
XmaI/EcoRI
DIGESTION
BglII
XmaI
AflII
NheI
BstXI
EcoRI
pB1
BamHI

FIG. 19D

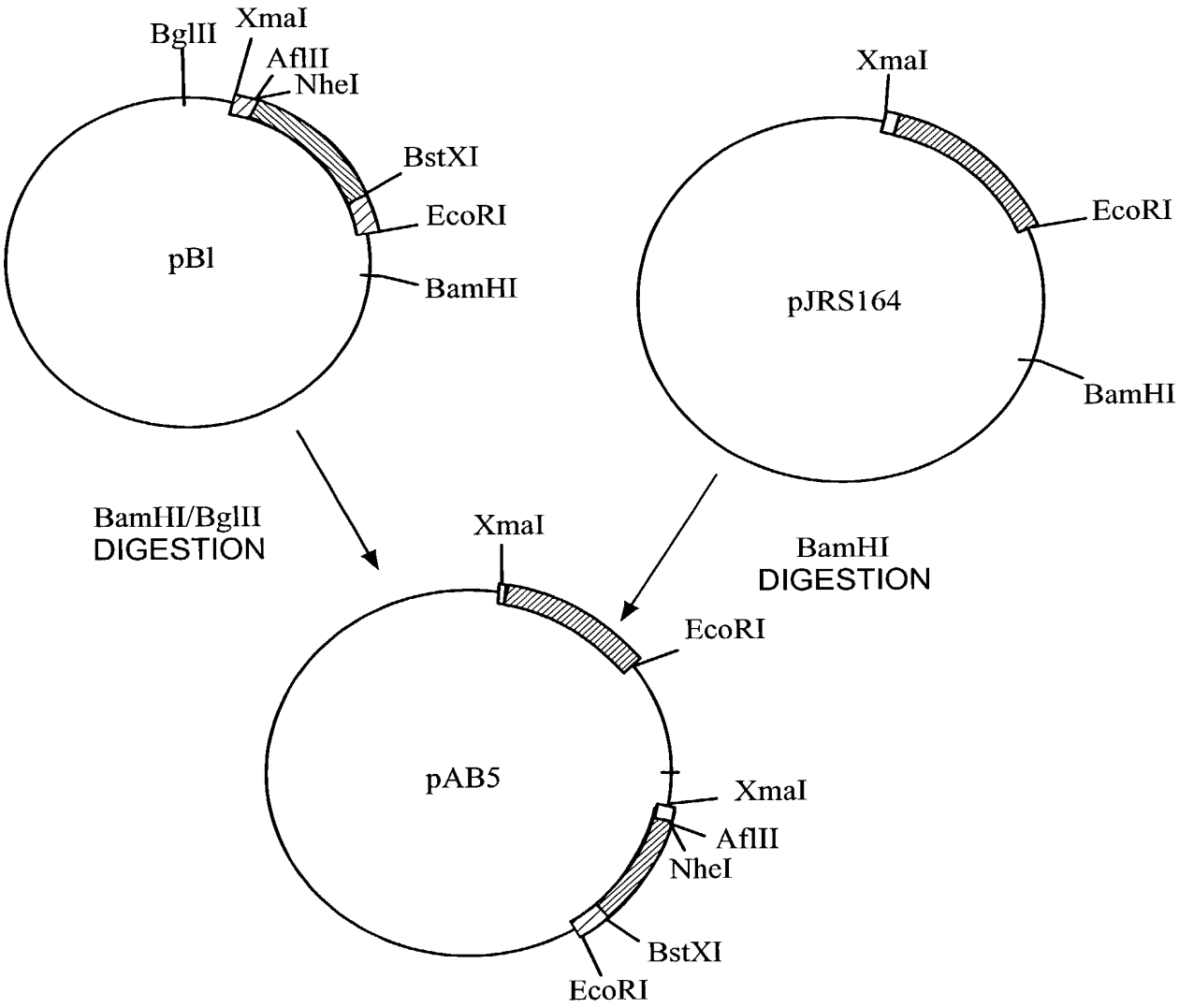
BglII
XmaI
AflII
NheI
BstXI
EcoRI
pBl
BamHI
XmaI
EcoRI
pJRS164
BamHI
BamHII/BglII
DIGESTION
BamHI
DIGESTION
XmaI
EcoRI
pAB5
XmaI
AflII
NheI
BstXI
EcoRI

FIG. 19E

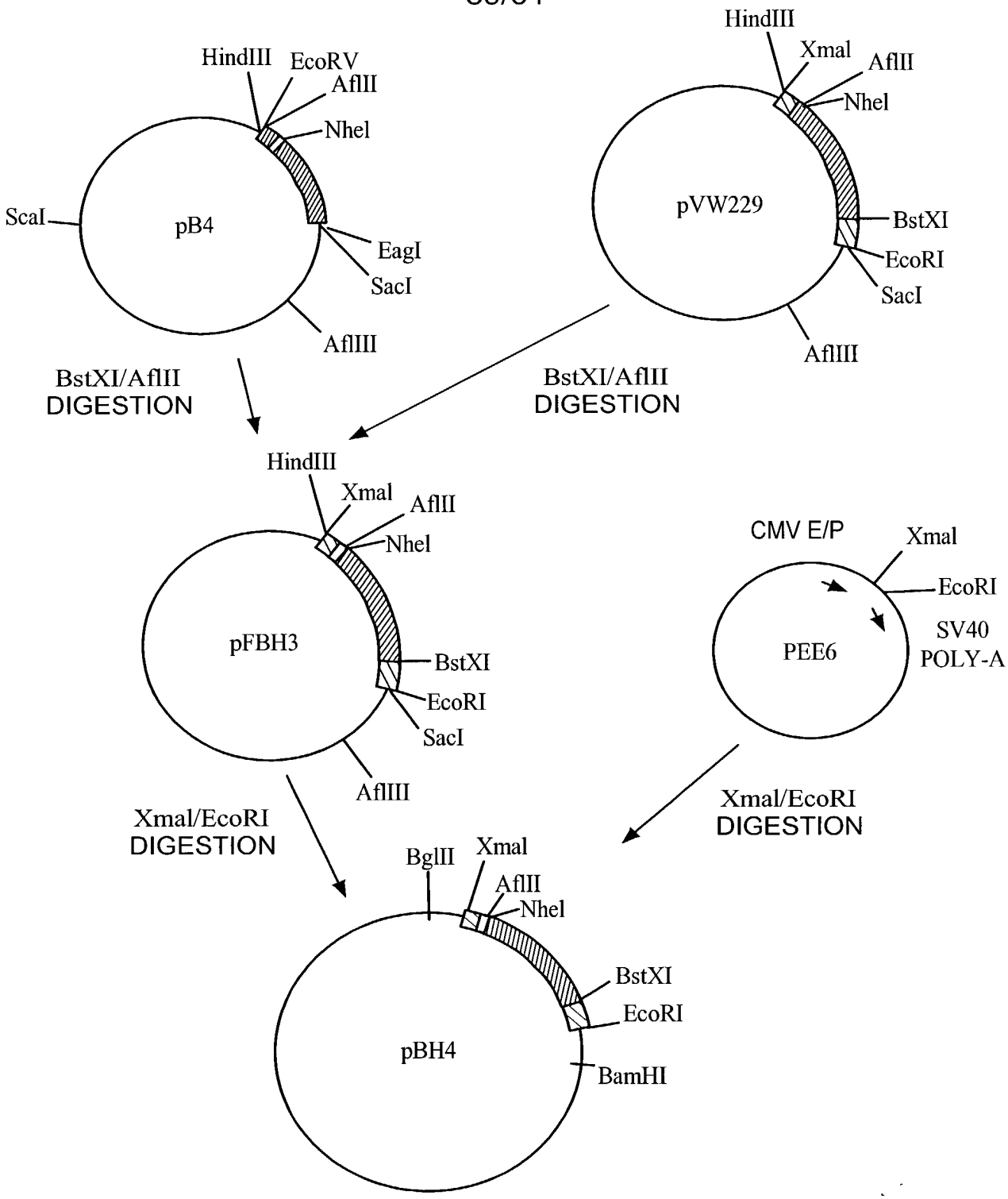
HindIII
EcoRV
AflII
NheI
ScaI
pB4
EagI
SacI
AflIII
BstXI/AflII
DIGESTION
HindIII
XmaI
AflII
NheI
pVW229
BstXI
EcoRI
SacI
AflIII
BstXI/AflII
DIGESTION
HindIII
XmaI
AflII
NheI
pFBH3
BstXI
EcoRI
SacI
AflIII
CMV E/P
XmaI
EcoRI
SV40
POLY-A
PEE6
XmaI/EcoRI
DIGESTION
XmaI/EcoRI
DIGESTION
BglII
XmaI
AflII
NheI
BstXI
EcoRI
pBH4
BamHI

FIG. 19F

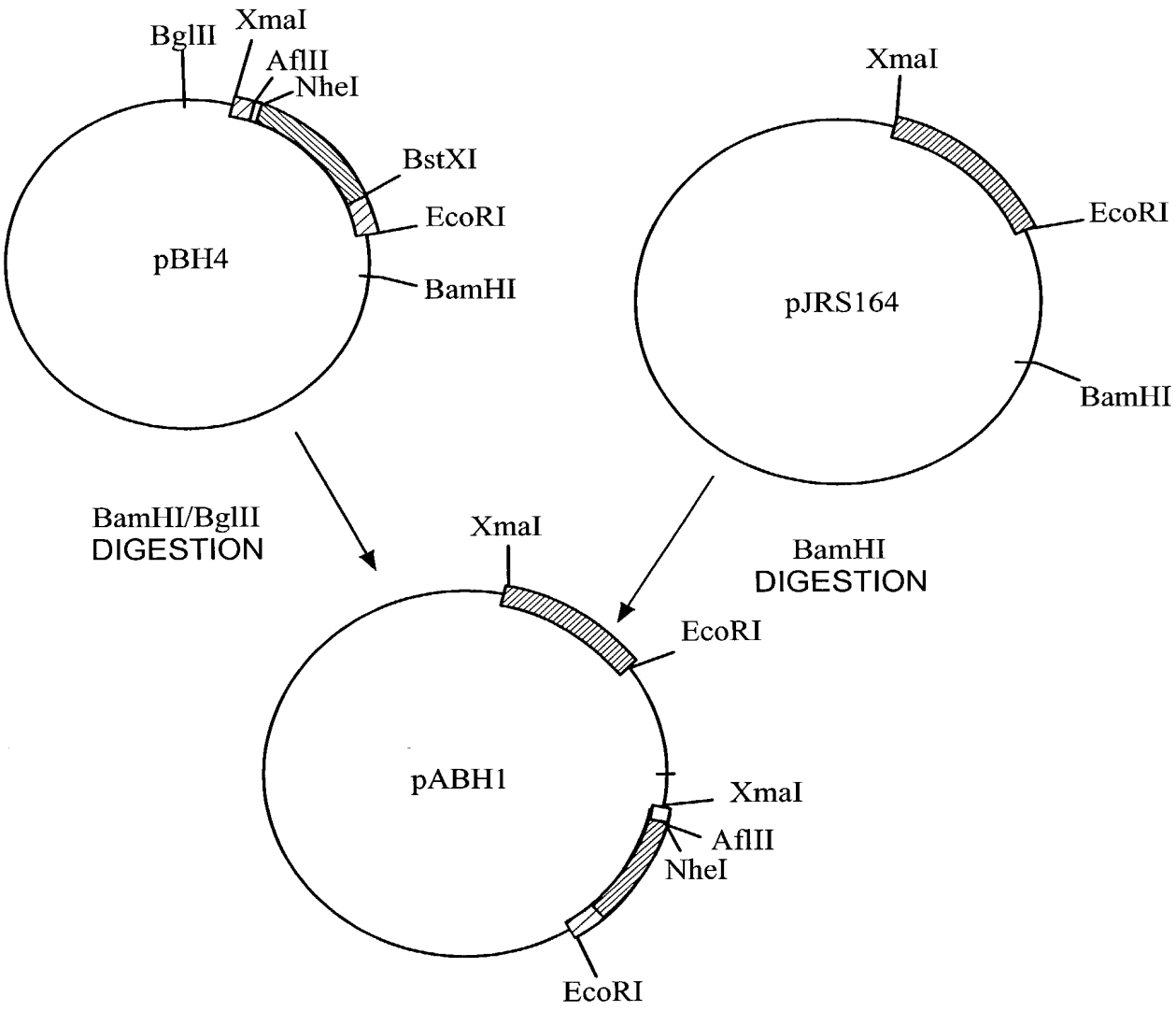
BglII
XmaI
AflII
NheI
BstXI
EcoRI
pBH4
BamHI
XmaI
EcoRI
pJRS164
BamHI
BamHI/BglII
DIGESTION
XmaI
BamHI
DIGESTION
EcoRI
pABH1
XmaI
AflII
NheI
EcoRI

FIG. 19G

OLIGONUCLEOTIDES USED IN CLONING

OPR132

I-A^d β SIGNAL PEPTIDE FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- HindIII/Xmal SITES

5' -CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA GC-3'

OPR133

I-A^d β SIGNAL PEPTIDE BACK PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- AflII SITE

5' -CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

I-A^d β TRANSMEMBRANE FRONT PRIMER FOR CellTech VECTOR- BstXI SITES

5' -CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

I-A^d β TRANSMEMBRANE BACK PRIMER FOR CellTech VECTOR- SstI, EcoRI SITES

5' -CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'

OPR136

I-A^d a SIGNAL PEPTIDE FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- HindIII/Xmal SITES

5' -CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC TG-3'

OPR139

I-A^d α TRANSMEMBRANE PRIMER FOR CellTech VECTOR- SstI/EcoRI SITES

5' -CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'

B7-1-2F

MURINE B7-1 FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- NotI SITES

5' -CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT C-3'

B7-1-2B

MURINE B7-1 BACK PRIMER FOR CellTech VECTOR- NotI SITE

5' -CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

FIG. 20

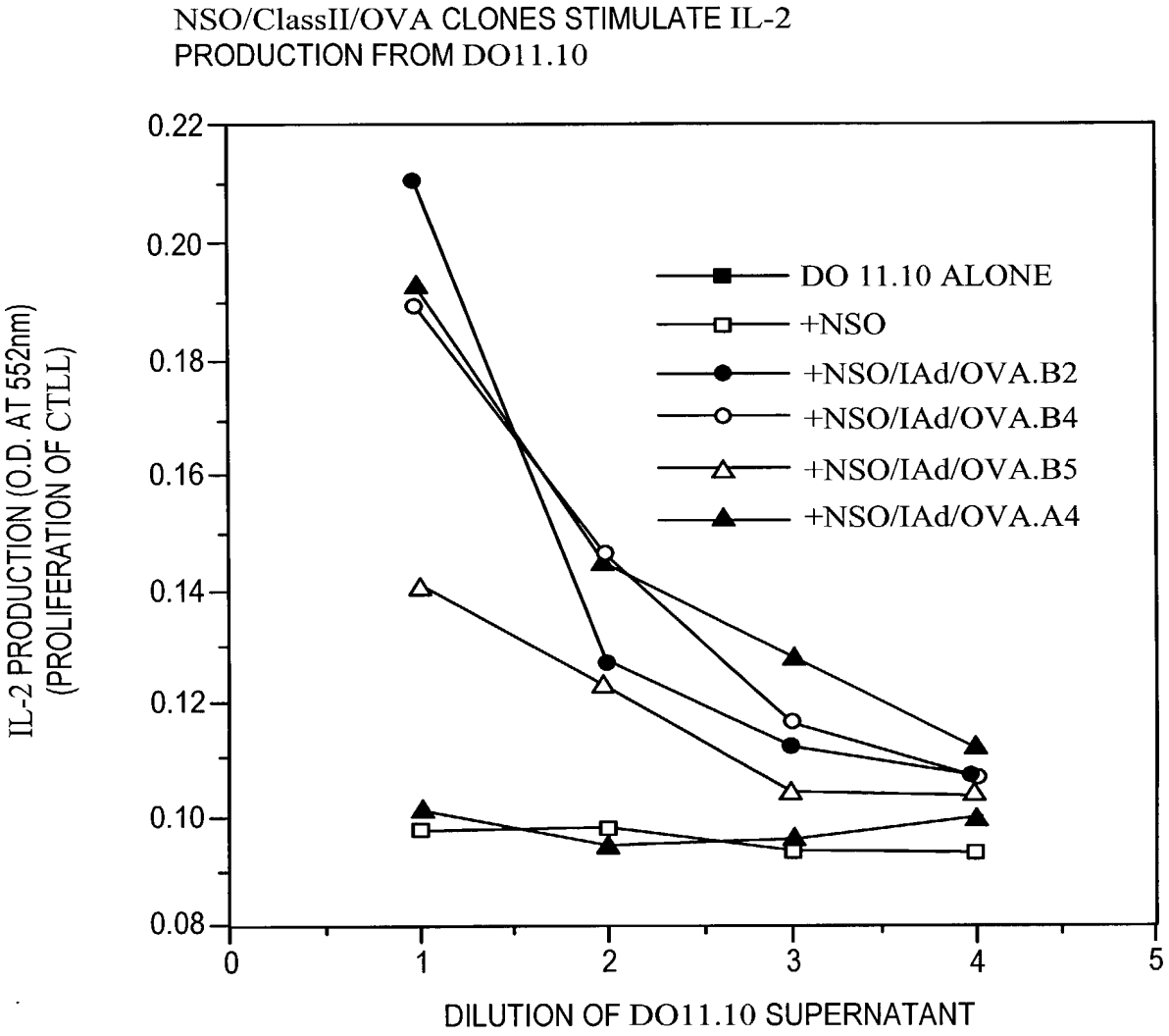
NSO/ClassII/OVA CLONES STIMULATE IL-2 PRODUCTION FROM DO11.10
IL-2 PRODUCTION (O.D. AT 552nm) (PROLIFERATION OF CTLL)
0.22
0.20
0.18
0.16
0.14
0.12
0.10
0.08
0
1
2
3
4
5
DILUTION OF DO11.10 SUPERNATANT
DO 11.10 ALONE
+NSO
+NSO/IAd/OVA.B2
+NSO/IAd/OVA.B4
+NSO/IAd/OVA.B5
+NSO/IAd/OVA.A4

FIG. 21

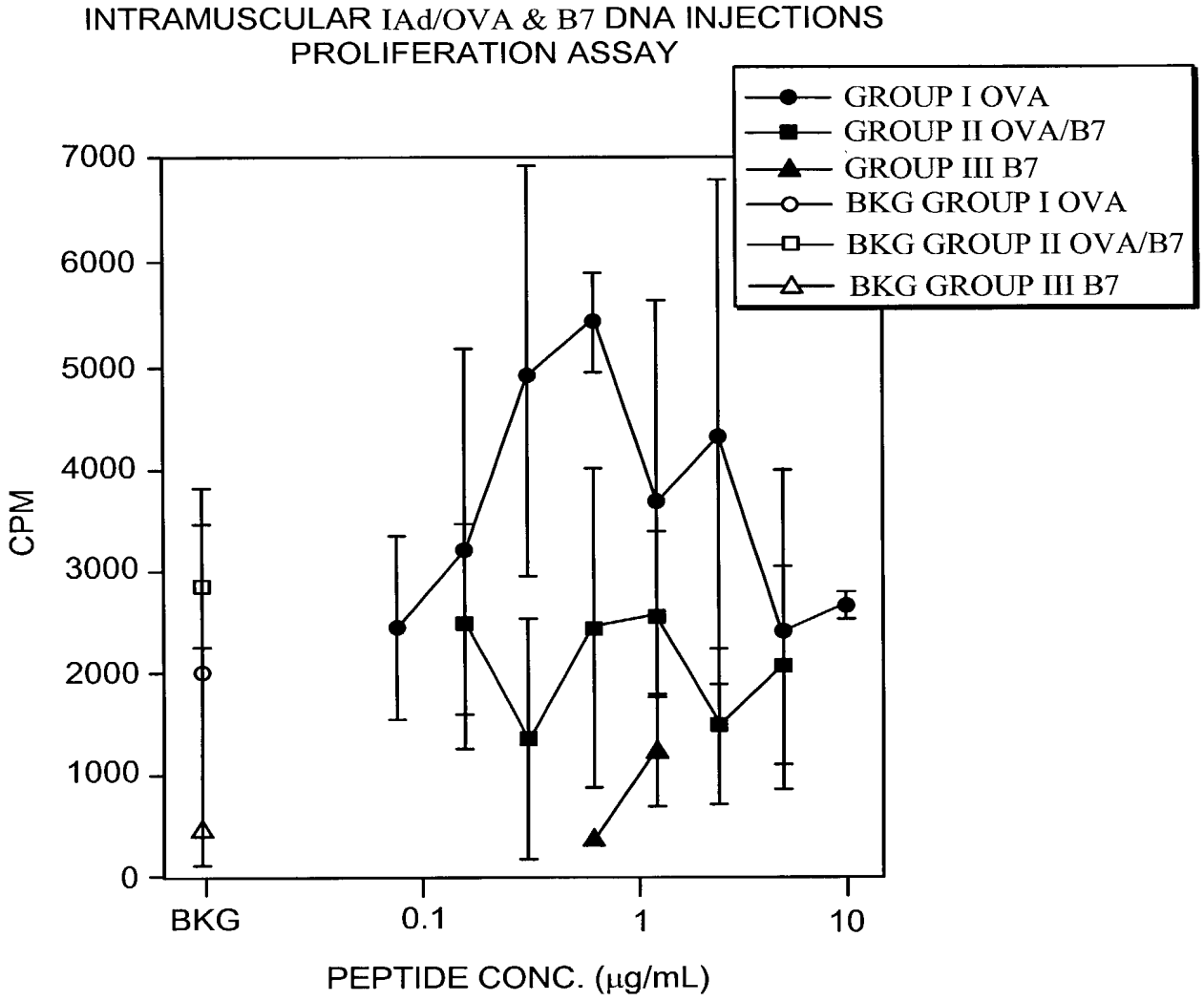
INTRAMUSCULAR IAd/OVA & B7 DNA INJECTIONS
PROLIFERATION ASSAY
GROUP I OVA
GROUP II OVA/B7
GROUP III B7
BKG GROUP I OVA
BKG GROUP II OVA/B7
BKG GROUP III B7
CPM
7000
6000
5000
4000
3000
2000
1000
0
BKG
0.1
1
10
PEPTIDE CONC. (µg/mL)

FIG. 22

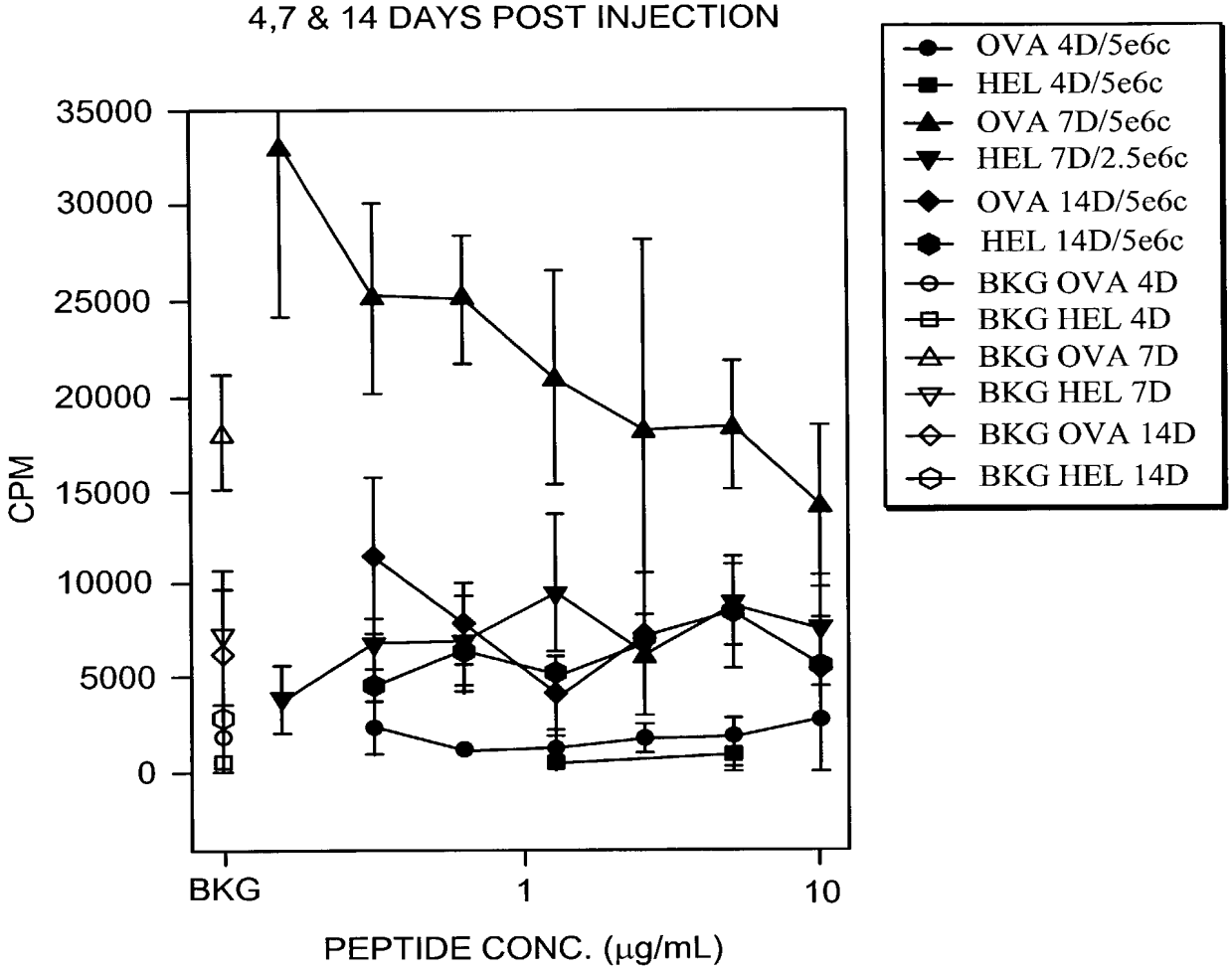
INTRADERMAL IAd/OVA & IAd/HEL DNA INJECTIONS
PROLIFERATION ASSAY
4,7 & 14 DAYS POST INJECTION
OVA 4D/5e6c
HEL 4D/5e6c
OVA 7D/5e6c
HEL 7D/2.5e6c
OVA 14D/5e6c
HEL 14D/5e6c
BKG OVA 4D
BKG HEL 4D
BKG OVA 7D
BKG HEL 7D
BKG OVA 14D
BKG HEL 14D
CPM
35000
30000
25000
20000
15000
10000
5000
0
BKG
1
10
PEPTIDE CONC. (µg/mL)

FIG. 23

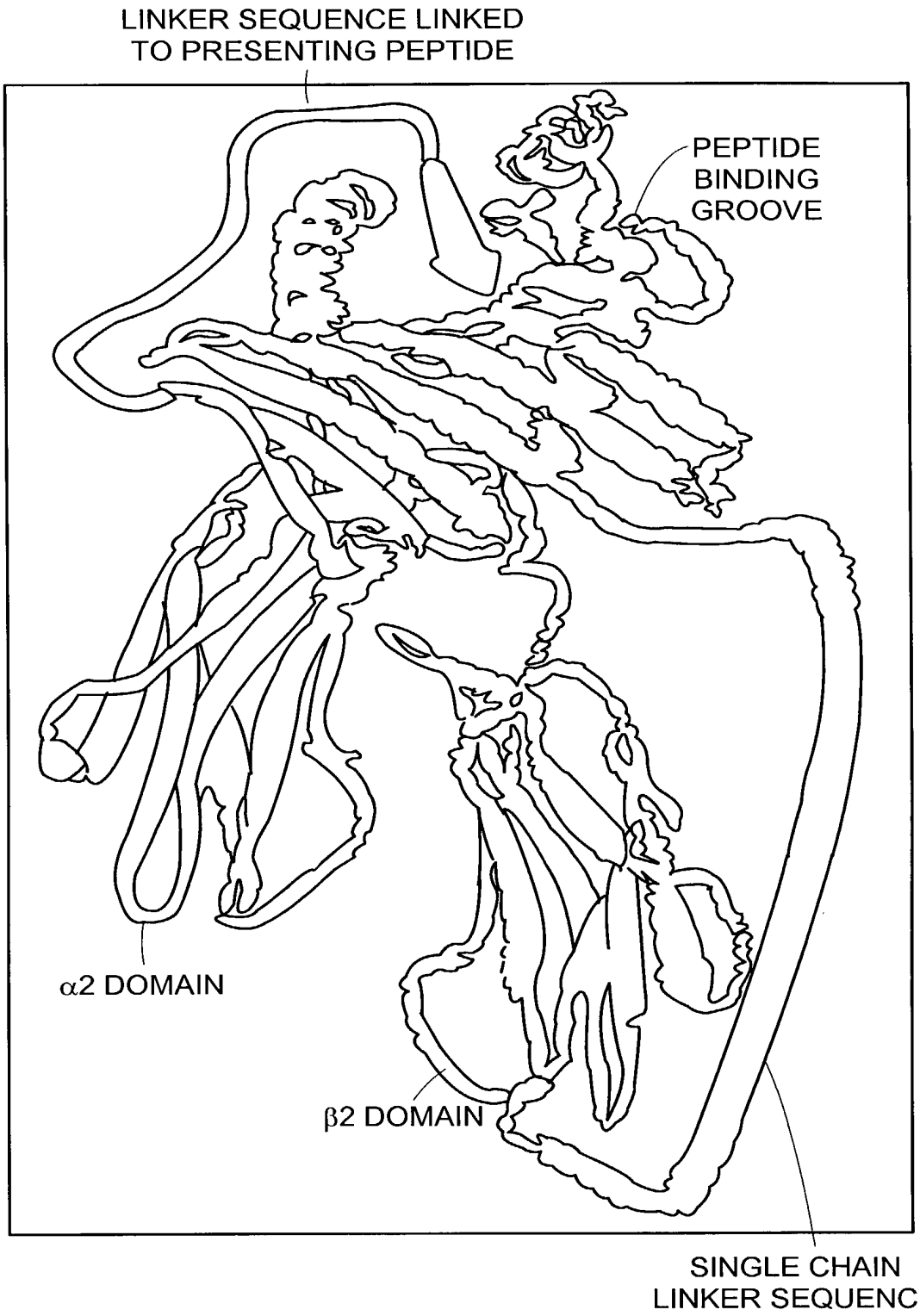
LINKER SEQUENCE LINKED
TO PRESENTING PEPTIDE
PEPTIDE
BINDING
GROOVE
α2 DOMAIN
β2 DOMAIN
SINGLE CHAIN
LINKER SEQUENCE

FIG. 24

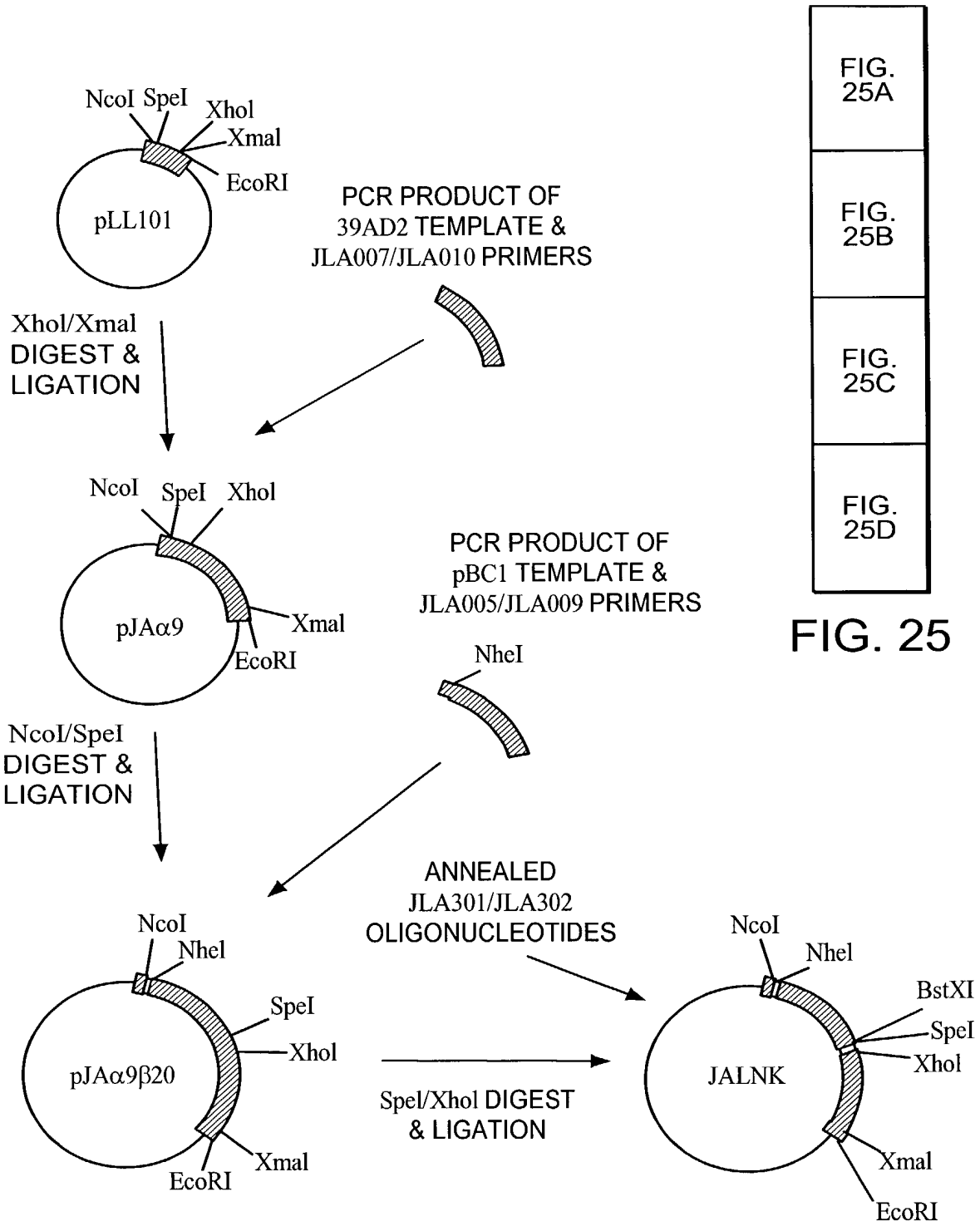

FIG. 25A
FIG. 25B
FIG. 25C
FIG. 25D

FIG. 25

FIG. 25A

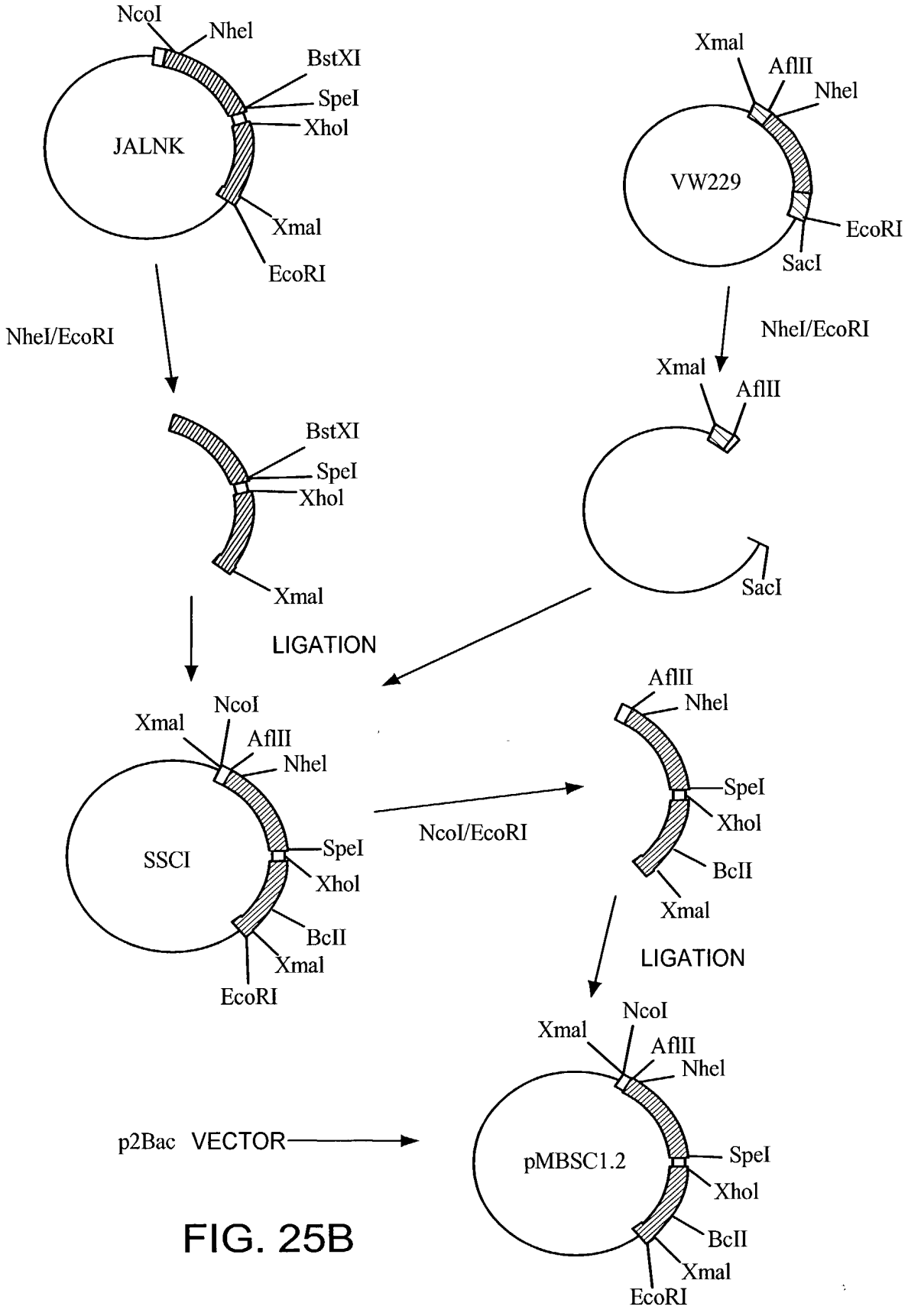
NcoI
NheI
BstXI
SpeI
XhoI
JALNK
XmaI
EcoRI
NheI/EcoRI
BstXI
SpeI
XhoI
XmaI
XmaI
AflII
NheI
VW229
EcoRI
SacI
NheI/EcoRI
XmaI
AflII
SacI
LIGATION
AflII
NheI
SpeI
XhoI
BclI
XmaI
LIGATION
XmaI
NcoI
AflII
NheI
SpeI
XhoI
BclI
XmaI
EcoRI
NcoI/EcoRI
p2Bac VECTOR
XmaI
NcoI
AflII
NheI
pMBSC1.2
SpeI
XhoI
BclI
XmaI
EcoRI

FIG. 25B

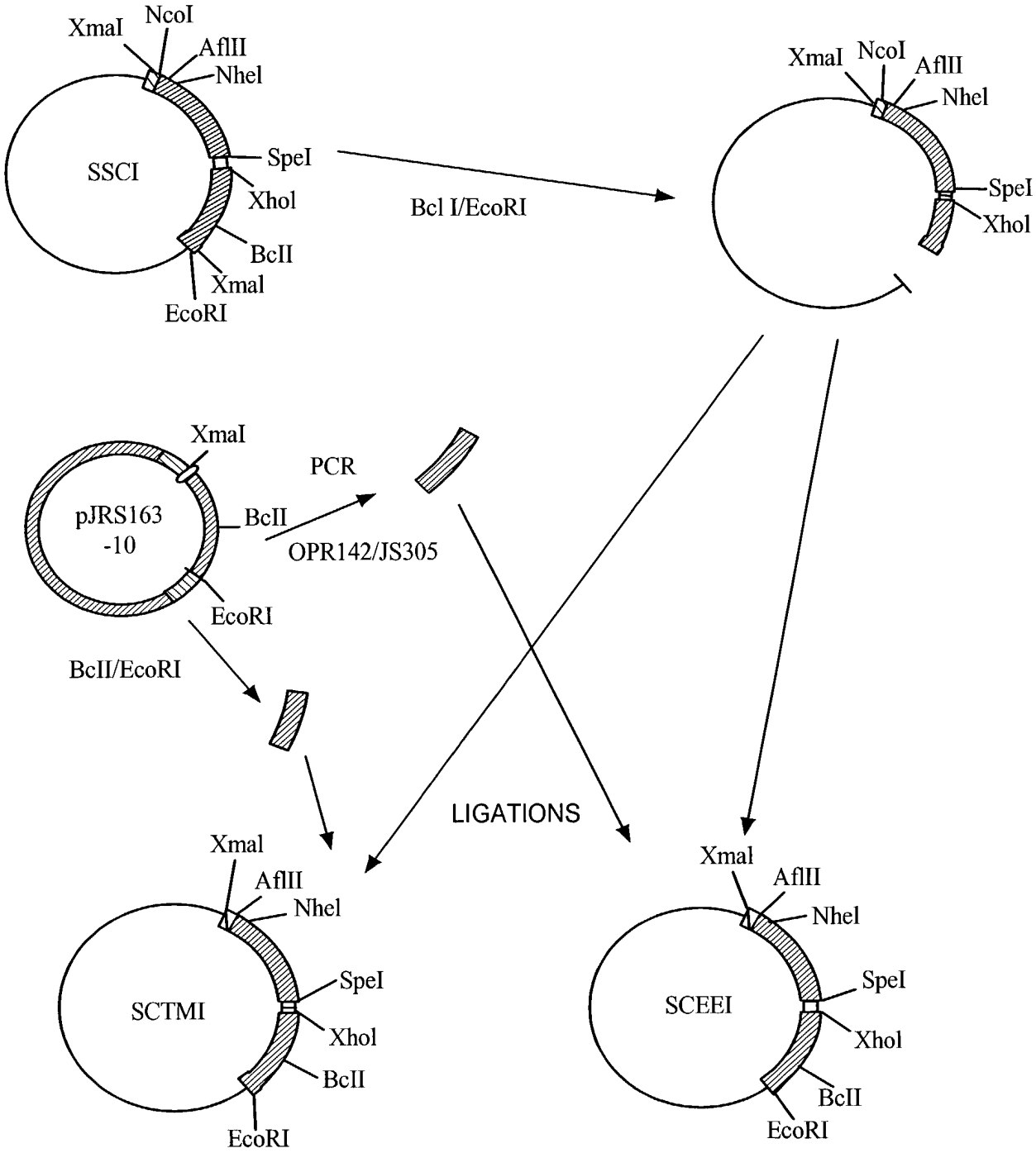
XmaI
NcoI
AflII
NheI
SpeI
XhoI
BclII
XmaI
EcoRI
SSCI
Bcl I/EcoRI
XmaI
NcoI
AflII
NheI
SpeI
XhoI
XmaI
pJRS163
-10
BclII
EcoRI
PCR
OPR142/JS305
BclII/EcoRI
LIGATIONS
XmaI
AflII
NheI
SpeI
XhoI
BclII
EcoRI
SCTMI
XmaI
AflII
NheI
SpeI
XhoI
BclII
EcoRI
SCEEI

FIG. 25C

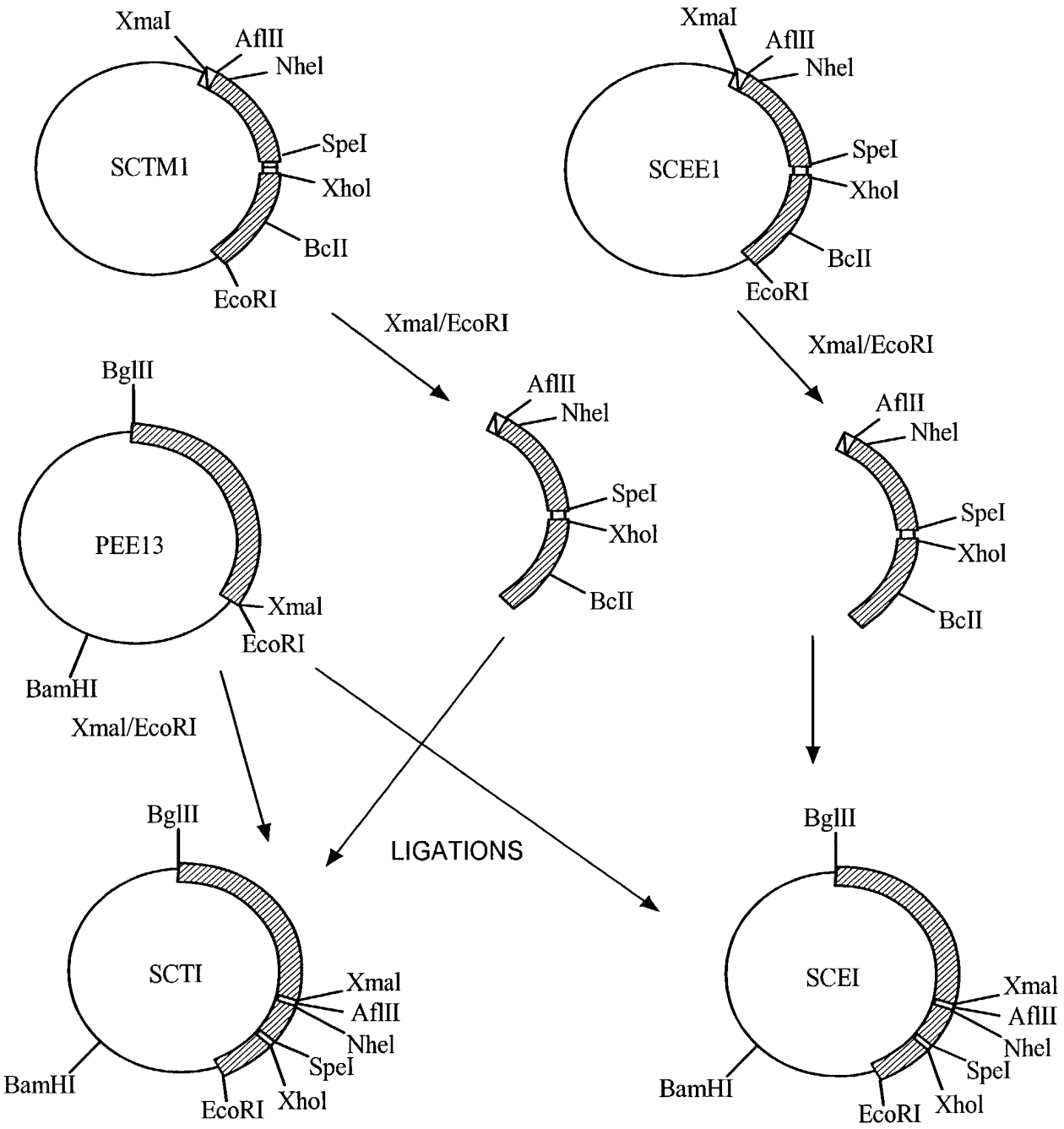
XmaI
AflII
NheI
SCTM1
SpeI
XhoI
BcII
EcoRI
XmaI/EcoRI
XmaI
AflII
NheI
SCEE1
SpeI
XhoI
BcII
EcoRI
XmaI/EcoRI
BglII
PEE13
XmaI
EcoRI
BamHI
XmaI/EcoRI
AflII
NheI
SpeI
XhoI
BcII
AflII
NheI
SpeI
XhoI
BcII
LIGATIONS
BglII
SCTI
XmaI
AflII
NheI
SpeI
XhoI
EcoRI
BamHI
BglII
SCEI
XmaI
AflII
NheI
SpeI
XhoI
EcoRI
BamHI

FIG. 25D

JLA-005

5' -CCCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007

5' -CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009

5' -CCCCCCACTAGTCCACTCCACAGTGATGGGGCT-3'

JLA-010

5' -CCCCCCCCCCGGGACCAGTGTTTCAGAACCGGCTCCTC-3'

JLA-301

5' -TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-
ACCACCACCGCCGCTGCCACCGCCACCA-3'

JLA-302

5' -CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTTCCGG-
TGGCGGCGGTTCTGGCGGTGGCGGTTCC-3'

OPR-142

5' -CTTGGGAATCTTGACTAAGAGG-3'

JS-305

5' -CAGGTCGAATTCTCATTCCATCGGCATGTACTCTTCTT-
CCTCCCAGTGTTTCAGAACCGG-3'

FIG. 26

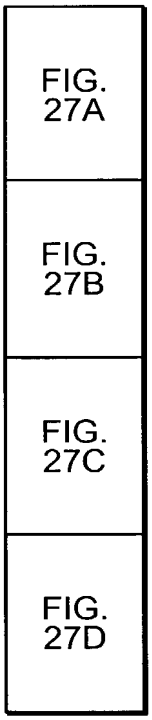

FIG. 27

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

FIG. 27A


```
          10          20          30          40          50
           *           *           *           *           *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M   A   L   Q   I   P   S   L   L   L   S   A   A   V   V>
     <---------------------  I-Ad β CHAIN LEADER  ------------------------

          60          70          80          90
           *           *           *           *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
 V   L   M   V   L   S   S   P   R   T   L   S   I   S   Q   A>
-------------------------------------------------------------><----------------

100         110         120         130         140
 *           *           *           *           *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
 V   H   A   A   H   A   E   I   N   E   A   G   R   A   S   G>
--------- OVA 323-339 ----------------------------------------><----------------

 150         160         170         180         190
  *           *           *           *           *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
 G   G   G   S   G   G   G   G   N   S   E   R   H   F   V   V>
-- 10 AMINO ACID LINKER --><--------  I-Ad β-1 DOMAIN ------------

    200         210         220         230         240
     *           *           *           *           *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
 Q   F   K   G   E   C   Y   Y   T   N   G   T   Q   R   I   R>
-------------------------------------------------------------------------------

        250         260         270         280         290
         *           *           *           *           *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
 L   V   T   R   Y   I   Y   N   R   E   E   Y   V   R   Y   D>
-------------------------------------------------------------------------------

          300         310         320         330
           *           *           *           *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
 S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D>
-------------------------------------------------------------------------------

340         350         360         370         380
 *           *           *           *           *
GCC GAG TAC TGG AAC AGC CAG CCC GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
 A   E   Y   W   N   S   Q   P   E   I   L   E   R   T   R   A>
-------------------------------------------------------------------------------
```

FIG. 27B

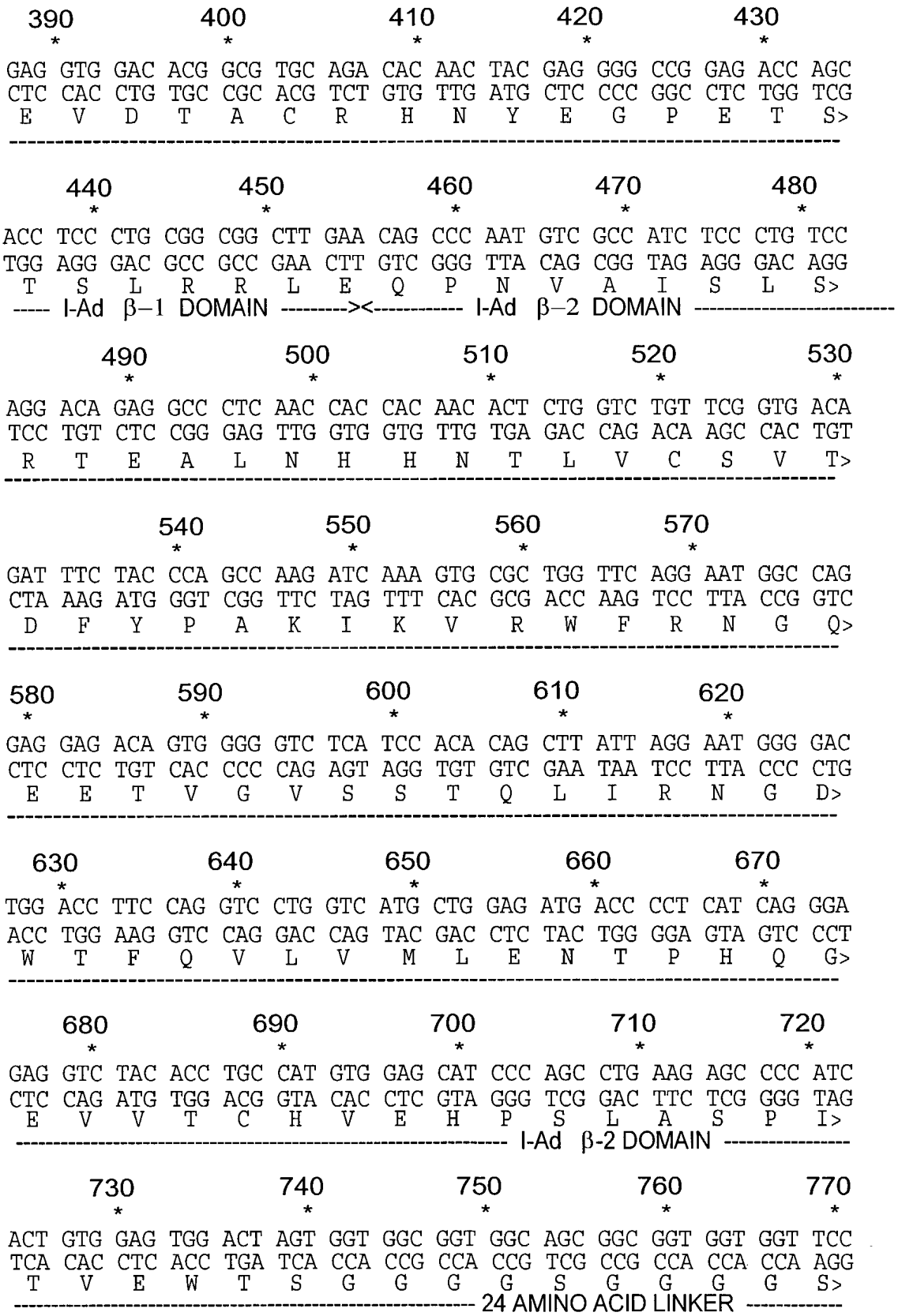
390 400 410 420 430
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>
440 450 460 470 480
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>
----- I-Ad β–1 DOMAIN --------><---------- I-Ad β–2 DOMAIN ----------
490 500 510 520 530
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>
540 550 560 570
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>
580 590 600 610 620
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>
630 640 650 660 670
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
W T F Q V L V M L E N T P H Q G>
680 690 700 710 720
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
E V V T C H V E H P S L A S P I>
---------- I-Ad β-2 DOMAIN ----------
730 740 750 760 770
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TCA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T V E W T S G G G G S G G G G S>
---------- 24 AMINO ACID LINKER ----------

FIG. 27C


```
                780         790         800         810
                 *           *           *           *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCC ACT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-------------------------------------------------------------><----------

820         830         840         850         860
 *           *           *           *           *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
-------- I-Ad α-1 DOMAIN ----------------------------------------------------

870         880         890         900         910
 *           *           *           *           *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTC TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
-----------------------------------------------------------------------------

920         930         940         950         960
 *           *           *           *           *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y   V   D   L   D   K   K   K   T   V   W   R   L   P   E   F>
-----------------------------------------------------------------------------

970         980         990         1000        1010
 *           *           *           *           *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
-----------------------------------------------------------------------------

                1020        1030        1040        1050
                 *           *           *           *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
---------------------------------------------------------- I-Ad α-1 DOMAIN ----------

1060        1070        1080        1090        1100
 *           *           *           *           *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
----------------------><--------- I-Ad α-2 DOMAIN ----------------------------------

1110        1120        1130        1140        1150
 *           *           *           *           *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   T>
-----------------------------------------------------------------------------
```

```
    1160          1170          1180          1190          1200
     *             *             *             *             *
TTC CCA GCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACG GAG TCT TTA TCG TTC AGT CAG
 F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-------------------------------------------------------------------------------

      1210          1220          1230          1240          1250
       *             *             *             *             *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H   S>
-------------------------------------------------------------------------------

          1260          1270          1280          1290
           *             *             *             *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-------------------------------------------------------------------------------

1300          1310          1320          1330          1340
 *             *             *             *             *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   K>
------------------------------------------------------------ I-Ad α-2 DOMAIN ----------

 1350          1360          1370          1380
  *             *             *             *
CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG
GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTA GTG ATC
 H   W   S   R   A   S   H   H   H   H   H   H   *>
---------><---------------------------- 6 X HIS TAG------->
```

FIG. 27D

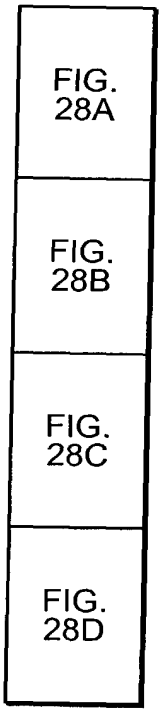

FIG. 28

FIG. 28A

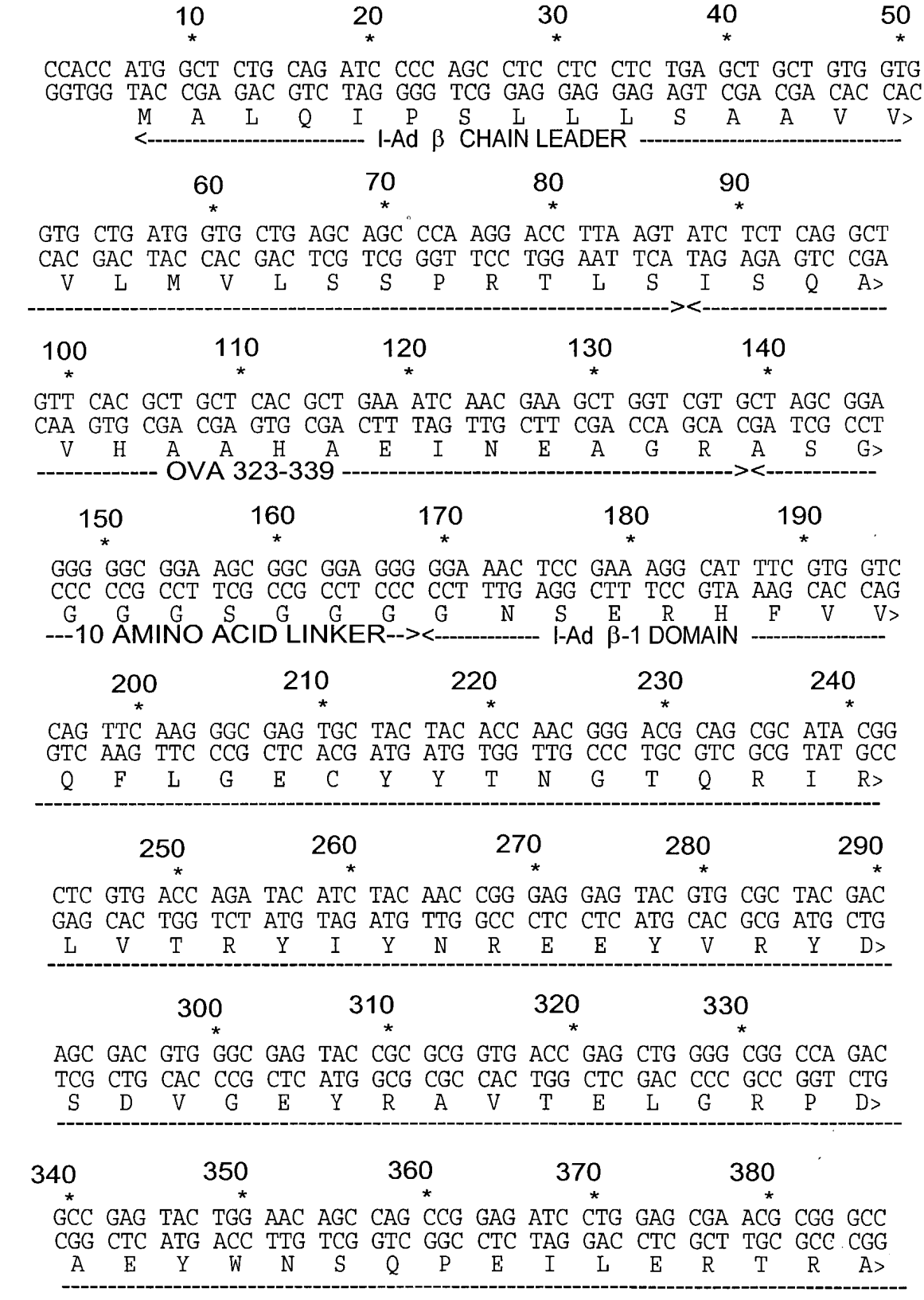
10 20 30 40 50
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TGA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
M A L Q I P S L L L S A A V V>
I-Ad β CHAIN LEADER
60 70 80 90
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V L M V L S S P R T L S I S Q A>
100 110 120 130 140
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
V H A A H A E I N E A G R A S G>
OVA 323-339
150 160 170 180 190
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
G G G S G G G G N S E R H F V V>
---10 AMINO ACID LINKER--><---------- I-Ad β-1 DOMAIN ----------
200 210 220 230 240
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
Q F L G E C Y Y T N G T Q R I R>
250 260 270 280 290
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
L V T R Y I Y N R E E Y V R Y D>
300 310 320 330
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
S D V G E Y R A V T E L G R P D>
340 350 360 370 380
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
A E Y W N S Q P E I L E R T R A>

FIG. 28B


```
      390         400         410         420         430
       *           *           *           *           *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
 E   V   D   T   A   C   R   H   N   Y   E   G   P   E   T   S>
-------------------------------------------------------------------------------------------------

      440         450         460         470         480
       *           *           *           *           *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
 T   S   L   R   R   L   E   Q   P   N   V   A   I   S   L   S>
---- I-Ad β-1 DOMAIN --------><---------- I-Ad β-2 DOMAIN ----------------------

      490         500         510         520         530
       *           *           *           *           *
AGG ACA GAG GCC CTC AAG CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
 R   T   E   A   L   N   H   H   N   T   L   V   C   S   V   T>
-------------------------------------------------------------------------------------------------

      540         550         560         570
       *           *           *           *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
 D   F   Y   P   A   K   I   K   V   R   W   F   R   N   G   Q>
-------------------------------------------------------------------------------------------------

580         590         600         610         620
 *           *           *           *           *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
 E   E   T   V   G   V   S   S   T   Q   L   I   R   N   G   D>
-------------------------------------------------------------------------------------------------

      630         640         650         660         670
       *           *           *           *           *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
 W   T   F   Q   V   L   V   M   L   E   M   T   P   H   Q   G>
-------------------------------------------------------------------------------------------------

      680         690         700         710         720
       *           *           *           *           *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
 E   V   Y   T   C   H   V   E   H   P   S   L   K   S   P   I>
------------------------------------------------------- I-Ad β-2 DOMAIN ----------------------

      730         740         750         760         770
       *           *           *           *           *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
 T   V   E   W   T   S   G   G   G   G   S   G   G   G   G   S>
-------------------------------------------------------- 24 AMINO ACID LINKER---------
```

FIG. 28C

```
                780         790         800         810
                 *           *           *           *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-------------------------------------------------------------><----------

820         830         840         850         860
 *           *           *           *           *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E   A   D   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
------- I-Ad α-1 DOMAIN ----------------------------------------------------

870         880         890         900         910
 *           *           *           *           *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
-------------------------------------------------------------------------

920         930         940         950         960
 *           *           *           *           *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y   V   D   L   D   K   K   K   T   V   W   R   L   P   E   F>
-------------------------------------------------------------------------

970         980         990         1000        1010
 *           *           *           *           *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
-------------------------------------------------------------------------

1020        1030        1040        1050
 *           *           *           *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
------------------------------------------------------------ I-Ad α-1 DOMAIN --------

1060        1070        1080        1090        1100
 *           *           *           *           *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
------------------><-------- I-Ad α-2 DOMAIN ----------------------------------

1110        1120        1130        1140        1150
 *           *           *           *           *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   I>
-------------------------------------------------------------------------
```

```
1160        1170        1180        1190        1200
 *           *           *           *           *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTG
AAG GGT GGA CAC TAG TTG TAG TGT ACG GAG TCT TTA TCG TTC AGT CAG
  F   P   P   V   I   N   I   T   W   L   R   N   S   K   S   V>
-------------------------------------------------------------------------------------------------

      1210        1220        1230        1240        1250
        *           *           *           *           *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
  T   D   G   V   Y   E   T   S   F   L   V   N   R   D   H   S>
-------------------------------------------------------------------------------------------------

          1260        1270        1280        1290
            *           *           *           *
TTC CAC AAG CTG TCT TAT CTC ACG TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
  F   H   K   L   S   Y   L   T   F   I   P   S   D   D   D   I>
-------------------------------------------------------------------------------------------------

1300        1310        1320        1330        1340
 *           *           *           *           *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGG CAA GAC TTT
  Y   D   C   K   V   E   H   W   G   L   E   E   P   V   L   X>
------------------------------------------------------------ I-Ad α-2 DOMAIN ---------

  1350        1360        1370        1380        1390
    *           *           *           *           *
CAC TCG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT
GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA
  H   N   E   P   E   I   P   A   P   M   S   E   L   T   E   T>
 ---------><---------- I-Ad α-TM DOMAIN ----------------------------------------------------

    1400        1410        1420        1430        1440
      *           *           *           *           *
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC
  V   V   C   A   L   G   L   S   V   G   L   V   G   I   V   V>
-------------------------------------------------------------------------------------------------

        1450        1460        1470        1480        1490
          *           *           *           *           *
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA
CCG TGG TAG AAG TAG TAA GTT CCG GAG GCT AGT CCA CCG TGG AGG TCT
  G   T   I   F   I   I   Q   G   L   R   S   G   G   T   S   R>
-------------------------------------------------------------------------------------------------

          1500
            *
CAC CCA GGG CCT TTA TGA
GTG GGT CCC GGA AAT ACT
  H   P   G   P   L   *>
-- I-Ad α-TM DOMAIN ->
```

FIG. 28D

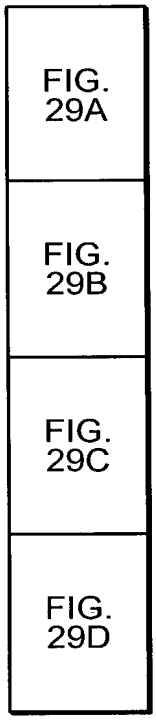

FIG. 29

FIG. 29A

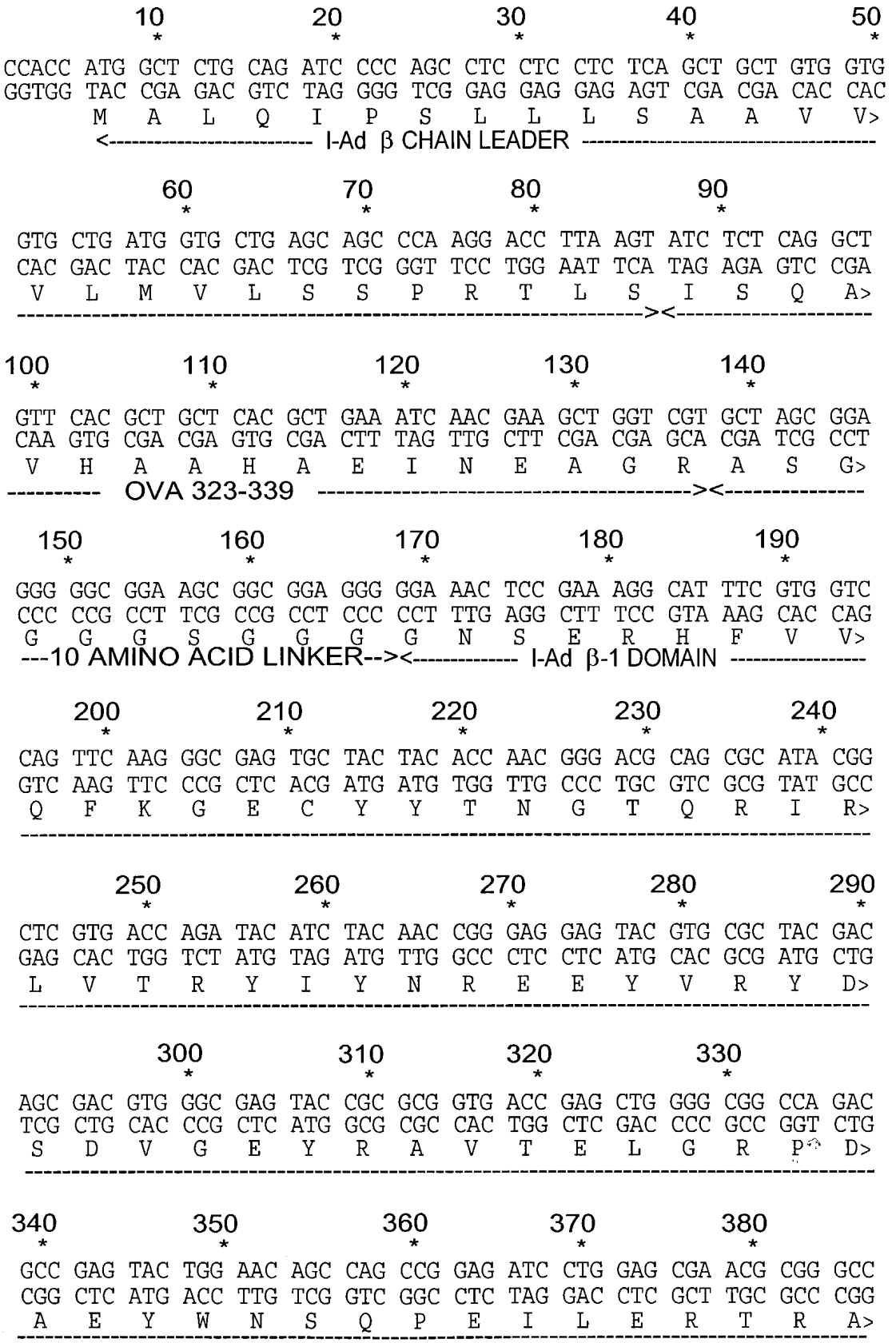
10 20 30 40 50
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
M A L Q I P S L L L S A A V V>
<---------- I-Ad β CHAIN LEADER ----------
60 70 80 90
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V L M V L S S P R T L S I S Q A>
100 110 120 130 140
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CGA GCA CGA TCG CCT
V H A A H A E I N E A G R A S G>
--------- OVA 323-339 ----------
150 160 170 180 190
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
G G G S G G G G N S E R H F V V>
---10 AMINO ACID LINKER--><---------- I-Ad β-1 DOMAIN ----------
200 210 220 230 240
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
Q F K G E C Y Y T N G T Q R I R>
250 260 270 280 290
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
L V T R Y I Y N R E E Y V R Y D>
300 310 320 330
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
S D V G E Y R A V T E L G R P D>
340 350 360 370 380
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
A E Y W N S Q P E I L E R T R A>

FIG. 29B

390 400 410 420 430

GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>

440 450 460 470 480

ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>
----- I-Ad β-1 DOMAIN -------><---------- I-Ad β-2 DOMAIN ----------

490 500 510 520 530

AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>

540 550 560 570

GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>

580 590 600 610 620

GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>

630 640 650 660 670

TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
W T F Q V L V M L F M T P H Q G>

680 690 700 710 720

GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
E V Y T C H V E H P S L K S P I>
---------- I-Ad β-2 DOMAIN ----------

730 740 750 760 770

ACT GTG GAG TGG ACT AGT GGT GGG GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T V E W T S G G G G S G G G G S>
----------><---------- 24 AMINO ACID LINKER----------

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

FIG. 29C


```
          780        790        800        810
           *          *          *          *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCC AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
 G   G   G   G   S   G   G   G   G   S   S   S   E   D   D   I>
-------------------------------------------------------------><----------

820        830        840        850        860
 *          *          *          *          *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
 E   A   C   H   V   G   F   Y   G   T   T   V   Y   Q   S   P>
------ I-Ad α-1 DOMAIN ----------------------------------------------------

 870        880        890        900        910
  *          *          *          *          *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
 G   D   I   G   Q   Y   T   H   E   F   D   G   D   E   L   F>
-----------------------------------------------------------------------------

  920        930        940        950        960
   *          *          *          *          *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
 Y   V   D   L   D   K   K   K   T   V   W   R   L   P   E   F>
-----------------------------------------------------------------------------

      970        980        990       1000       1010
       *          *          *          *          *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GSA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
 G   Q   L   I   L   F   E   P   Q   G   G   L   Q   N   I   A>
-----------------------------------------------------------------------------

          1020       1030       1040       1050
           *          *          *          *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
 A   E   K   H   N   L   G   I   L   T   K   R   S   N   F   T>
---------------------------------------------------------- I-Ad α-1 DOMAIN ----------

1060       1070       1080       1090       1100
 *          *          *          *          *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA CGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
 P   A   T   N   E   A   P   Q   A   T   V   F   P   K   S   P>
------------------><------ I-Ad α-2 DOMAIN ----------------------------------

 1110       1120       1130       1140       1150
  *          *          *          *          *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
 V   L   L   G   Q   P   N   T   L   I   C   F   V   D   N   I>
-----------------------------------------------------------------------------
```

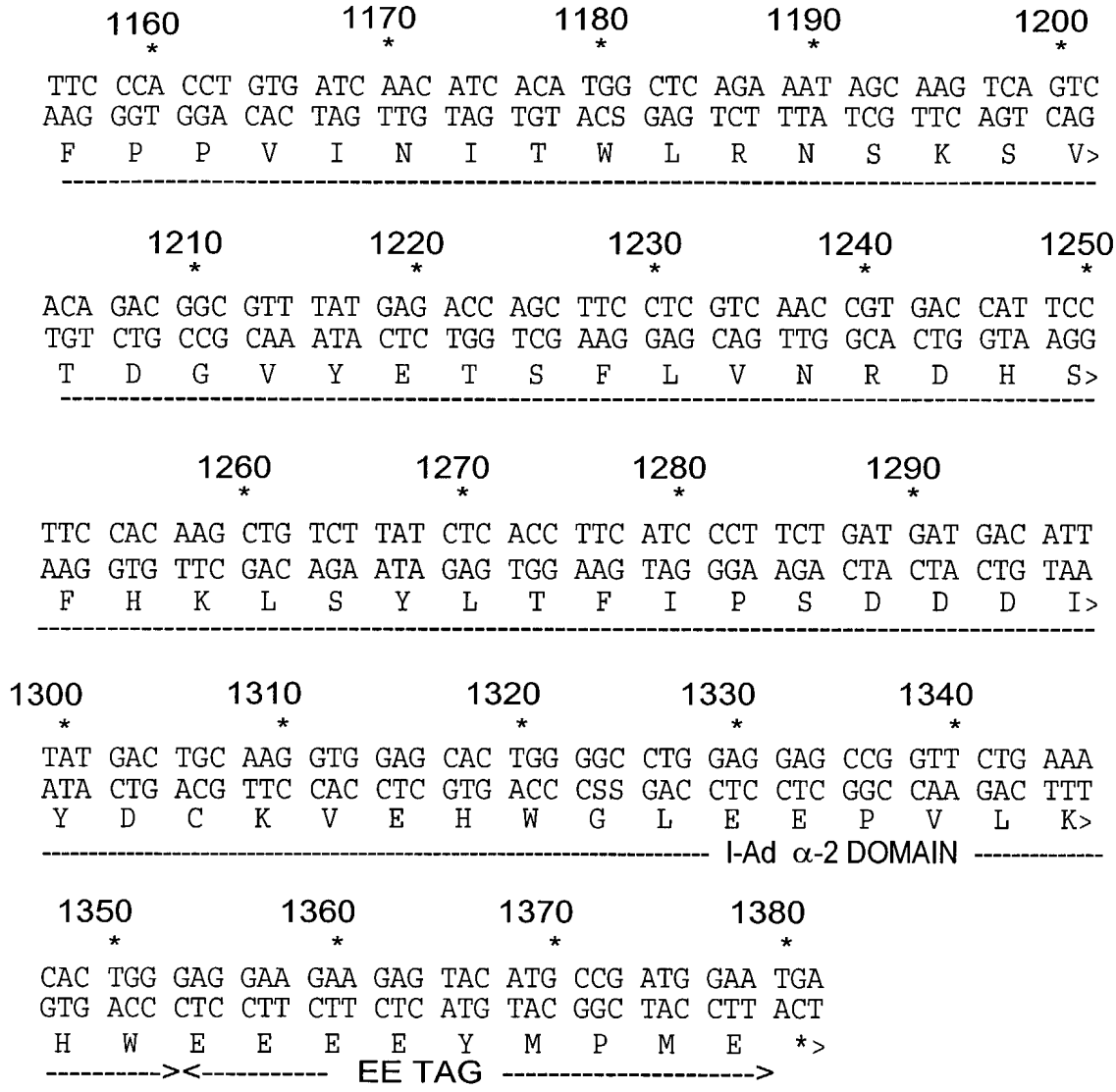
1160 1170 1180 1190 1200
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT GGA CAC TAG TTG TAG TGT ACS GAG TCT TTA TCG TTC AGT CAG
F P P V I N I T W L R N S K S V>
1210 1220 1230 1240 1250
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T D G V Y E T S F L V N R D H S>
1260 1270 1280 1290
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F H K L S Y L T F I P S D D D I>
1300 1310 1320 1330 1340
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CSS GAC CTC CTC GGC CAA GAC TTT
Y D C K V E H W G L E E P V L K>
I-Ad α-2 DOMAIN
1350 1360 1370 1380
CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA
GTG ACC CTC CTT CTT CTC ATG TAC GGC TAC CTT ACT
H W E E E E Y M P M E *>
><
EE TAG

FIG. 29D